

XX Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression
 XX
 PS Claim 32: Fig 7A; 53pp; English.
 XX
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)- κ B activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF- κ B
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,
 CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF- κ B expression and thus for drug
 CC designing.
 CC
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLOMAGCCSQNEYFDSLLHACIPQQLRCSSNTPPLTCQRYCNA SVTNSVGTNAIIMTCL 60
 Db 1 MLOMAGCCSQNEYFDSLLHACIPQQLRCSSNTPPLTCQRYCNA SVTNSVGTNAIIMTCL 60
 QY 61 GLSLIISLAVFVLMFLRKISSEPLKDEFNKNTSSGLGMANIDLEKSRGDEIILRGLE 120
 Db 61 GLSLIISLAVFVLMFLRKISSEPLKDEFNKNTSSGLGMANIDLEKSRGDEIILRGLE 120
 QY 121 YTYEECTCEDCIKSRKRVSDHCFPLPAMEGATIIYTTTNDYCKSLPALSATETEKS 180
 Db 121 YTYEECTCEDCIKSRKRVSDHCFPLPAMEGATIIYTTTNDYCKSLPALSATETEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184
 RESULT 2
 AAY94001 standard; Protein; 184 AA.
 XX
 AC AAY94001;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE A human BCMA protein, a B cell protein related to TACI.
 XX
 KW Human: BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchiolitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX
 OS Homo sapiens.
 XX
 PN WO200040716-A2.

XX
 PD 13-JUL-2000.
 XX
 XX 07-JAN-2000; 2000WO-US00396.
 PF
 XX 07-JAN-1999; 99US-0226533.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Gross JA, Xu W, Madden K, Yee DP;
 PI WPI: 2000-452538/39.
 DR N-PSDB: AAA58559.
 XX
 PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
 XX
 PS Disclosure: Page 152; 175pp; English.
 XX
 CC The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli.
 CC
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLOMAGCCSQNEYFDSLLHACIPQQLRCSSNTPPLTCQRYCNA SVTNSVGTNAIIMTCL 60
 Db 1 MLOMAGCCSQNEYFDSLLHACIPQQLRCSSNTPPLTCQRYCNA SVTNSVGTNAIIMTCL 60
 QY 61 GLSLIISLAVFVLMFLRKISSEPLKDEFNKNTSSGLGMANIDLEKSRGDEIILRGLE 120
 Db 61 GLSLIISLAVFVLMFLRKISSEPLKDEFNKNTSSGLGMANIDLEKSRGDEIILRGLE 120
 QY 121 YTYEECTCEDCIKSRKRVSDHCFPLPAMEGATIIYTTTNDYCKSLPALSATETEKS 180
 Db 121 YTYEECTCEDCIKSRKRVSDHCFPLPAMEGATIIYTTTNDYCKSLPALSATETEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184
 RESULT 3
 AAE09241
 ID AAE09241 standard; Protein; 184 AA.
 XX
 AC AAE09241;
 XX
 DT 19-NOV-2001 (first entry)
 XX

DE	Human BCMA protein.
XX	
KW	Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KV	TNFR; TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KX	psoriasis.
OS	Homo sapiens.
XX	
PN	MO200160397-A1.
XX	
PD	23-Aug-2001.
XX	
PF	28-Nov-2000; 2000WO-US323378.
XX	
PR	16-FEB-2000; 2000US-0182938.
PR	22-AUG-2000; 2000US-0226986.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Masters SA, Pittl RM;
PI	Yan M;
DR	WPI: 2001-541628/60.
XX	N-PSDB; AADI5902.
XX	
PT	Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT	activity, for treating autoimmune disorders and cancer, comprises
PT	exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT	antagonists -
XX	
PS	Example 2; Fig 2; 160pp; English.
XX	
CC	The invention relates to methods of using one or more agonists or
CC	antagonists to modulate the activity of the members of TNF (tumour
CC	necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC	e.g. TACI or BCMA. The method is useful for treating pathological
CC	conditions or diseases associated with increased TALL-1 and APRIL
CC	expression or activity. TALL-1 and APRIL antagonists are used to
CC	block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC	They are useful for treating a mammal suffering from cancer such
CC	as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC	autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC	psoriasis and lupus erythematosus. The present sequence is human
CC	BCMA protein.
XX	
SQ	Sequence 184 AA;
XX	
Query Match	100.0%; Score 964; DB 22; Length 184;
Best Local Similarity	100.0%; Pred. No. 1.3e-95;
Matches 184; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MIQMAGGCSQNRYEFSLLHACTIPCOLRGSSNPPLTCQRCAASTNSKGTNALIMTCL 60
Db	1 MIQMAGGCSQNRYEFSLLHACTIPCOLRGSSNPPLTCQRCAASTNSKGTNALIMTCL 60
OY	61 GLSLITISLAVFYAMPFLMKRISSEPKDKFNKGSGLGAMNIDLKESPRGDETILPRLGE 120
Db	61 GLSLITISLAVFYAMPFLMKRISSEPKDKFNKGSGLGAMNIDLKESPRGDETILPRLGE 120
OY	121 YTVECTCDECIKSAPKVDSDHCFFLPAMEEGATLLVTTKTNDYCKSLPALSAIEIKS 180
Db	121 YTVECTCDECIKSAPKVDSDHCFFLPAMEEGATLLVTTKTNDYCKSLPALSAIEIKS 180
OY	181 ISAR 184
Db	181 ISAR 184
RESULT 4	
AAE00506	
ID	AAE00506 standard; Protein: 184 AA.
XX	

AC	AA00506.	
XX		
DT	31-JUL-2001 (first entry)	
XX		
DE	Human B cell maturation protein (BCMA).	
XX		
KW	Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;	
KW	gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;	
KW	carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;	
KW	systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;	
KW	B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;	
KW	organ transplantation; HIV; human immunodeficiency virus; TNF;	
KW	tumour necrosis factor; BCMA; B cell maturation protein.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200124811-A1.	
XX		
PD	12-APR-2001.	
XX		
PF	05-OCT-2000; 2000WO-US27579.	
XX		
PR	06-OCT-1999; 99US-0157933.	
PR	11-PEB-2000; 2000US-0181807.	
PR	30-JUN-2000; 2000US-0215688.	
XX		
PA	(BIOJ) BIOGEN INC.	
PA	(APOT-) APOTECH R & D SA.	
XX		
PI	Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;	
DR	WPI; 2001-266242/27.	
DR	N-PSDB; AAD03844.	
XX		
PT	Treating a mammal for a condition associated with undesired cell	
PT	proliferation such as cancer or carcinoma, comprises administering a	
PT	composition comprising A Proliferation Inducing Ligand Receptor	
PT	(APRIL-R) antagonist	
XX		
PS	Claim 3; Fig 3A; 85pp; English.	
XX		
CC	The invention relates to a method of treating a mammal for a condition	
CC	associated with undesired cell proliferation such as cancer or	
CC	carcinoma. The method involves administering a composition comprising	
CC	A proliferation inducing ligand receptor (APRIL-R) also referred as	
CC	B cell maturation protein (BCM or BCMA) antagonist that antagonises the	
CC	interaction between APRIL and its cognate receptor(s). This method is	
CC	useful for treating undesired cell proliferation such as cancer or	
CC	carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,	
CC	prostate carcinoma, and other carcinomas whose proliferation is modulated	
CC	by APRIL. It is also useful for treating autoimmune diseases (Grave's	
CC	disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular	
CC	diseases, renal disorders, B-cell lympho-proliferative disorders,	
CC	immunosuppressive diseases, organ transplantation, inflammation and	
CC	human immunodeficiency virus (HIV), and for treating, suppressing or	
CC	altering an immune response involving a signalling pathway between	
CC	APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.	
CC	The present sequence is human APRIL-R also referred as BCMA or	
CC	BCM protein.	
XX		
XX		
SQ	Sequence 184 AA;	
	Query Match 100.0%; Score 964; DB 22; Length 184;	
	Best Local Similarity 100.0%; Pred. No. 1,3e-95;	
	Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYNCAVYNSVKGTAAILMTCL 60	
DB	1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYNCAVYNSVKGTAAILMTCL 60	
OY	61 GLSLIIISLAVFVPLMLLKRISSEPLKDEKFNKSGSLGAMANDLEKSRGDDIILPRGLE 120	
DB	61 GLSLIIISLAVFVPLMLLKRISSEPLKDEKFNKSGSLGAMANDLEKSRGDDIILPRGLE 120	

QY 121 YVVEECTCEDCIKSKPKVSDHCFPLPAMEGATILVTTKNDYCKSLPALSATIEIKS 180
 |||
 DB 121 YVVEECTCEDCIKSKPKVSDHCFPLPAMEGATILVTTKNDYCKSLPALSATIEIKS 180
 QY 181 ISAR 184
 |||
 DB 181 ISAR 184

RESULT 5
 AAB60698
 ID AAB60698 standard; Protein; 184 AA.
 XX
 AC AAB60698;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human BAFF receptor (BAFF-R).
 XX
 KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,
 PI Thompson J;
 DR WPI: 2001-202866/20.
 DR N-PSDB: AAF59998.
 XX
 PS Claim 20: Fig 1; 59pp; English.

The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R

CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAFF-R.
 XX
 SQ Sequence 184 AA:
 Query Match 100.0%; Score 964; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGCCSONEYFDSLHACIPQRCSSNFPPLTCQRCYCNASVYNSKGTAILMTCL 60
 |||
 DB 1 MLOMAGCCSONEYFDSLHACIPQRCSSNFPPLTCQRCYCNASVYNSKGTAILMTCL 60
 QY 61 GSLTIISLAVFVLMFLRKISSEPLKDERKNTGSGLLGMANIDLEKSRGDEITILPRGLE 120
 |||
 DB 61 GSLTIISLAVFVLMFLRKISSEPLKDERKNTGSGLLGMANIDLEKSRGDEITILPRGLE 120
 QY 121 YVVEECTCEDCIKSKPKVSDHCFPLPAMEGATILVTTKNDYCKSLPALSATIEIKS 180
 |||
 DB 121 YVVEECTCEDCIKSKPKVSDHCFPLPAMEGATILVTTKNDYCKSLPALSATIEIKS 180
 QY 181 ISAR 184
 |||
 DB 181 ISAR 184

RESULT 6
 AAY71979
 ID AAY71979 standard; Protein; 184 AA.
 XX
 AC AAY71979;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Human B cell maturation factor (BCMA) protein.
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Human necrosis factor and Apol-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; Rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..62
 FT /label= Extracellular_domain
 XX
 PN WO200068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12266.
 XX
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NME-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Shu HS;
 XX
 DR WPI: 2001-016094/02.
 DR N-PSDB: AAD02125.
 XX
 PI Isolated TALL-1 protein is used to identify compounds that regulate B

PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 XX
 PS Claim 37; Page 104-105; 112pp; English.
 XX
 XX The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues) and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16. In human tissues, BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.
 CC
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORCYNASTNSVKGKTNALIMTCL 60
 Db 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORCYNASTNSVKGKTNALIMTCL 60
 QY 61 GLSLIISLAVFVLMFLKRISEPLKDEFKNTGSLGMANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIISLAVFVLMFLKRISEPLKDEFKNTGSLGMANIDLEKSTGDEIILPRGLE 120
 QY 121 YVEECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPALASATEIEKS 180
 Db 121 YVEECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPALASATEIEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184

XX
 OS Homo sapiens.
 XX
 XX WO200238766-A2.
 PN
 XX
 PD 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001WO-US47018.
 PR
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PI
 PI Gross JA, Xu W, Henne RM, Grant FJ;
 DR WPI: 2002-508212/54.
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 FT Ztnfr12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 PS Disclosure; Page 135-136; 154pp; English.
 XX
 XX The present invention describes a human tumour necrosis factor receptor
 CC designated ztnfr12 (1). (1) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (1) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (1) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (1) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 23; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORCYNASTNSVKGKTNALIMTCL 60
 Db 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORCYNASTNSVKGKTNALIMTCL 60
 QY 61 GLSLIISLAVFVLMFLKRISEPLKDEFKNTGSLGMANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIISLAVFVLMFLKRISEPLKDEFKNTGSLGMANIDLEKSTGDEIILPRGLE 120
 QY 121 YVEECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPALASATEIEKS 180
 Db 121 YVEECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPALASATEIEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184

RESULT 8

AAE15484
ID AAE15484 standard: protein: 181 AA.
XX
XX AAE15484;
AC
XX
XX 12-MAR-2002 (first entry)
DE Human B-cell maturation (BCMA) protein.
XX
XX Human: transmembrane activator and intracellular CAML interactor; TACI;
KW cystostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immunodeficiency; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT 5..38
FT /note= "Cysteine-rich consensus region; This is region
FT is specifically claimed as SEQ ID NO: 7 in claim 1 of
FT the specification"
FT
FT Domain 52..72
FT /label= Transmembrane_domain
XX
XX WO200187979-A2.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX
XX 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
PI
XX
XX WPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX
XX Disclosure: Fig 10A; 9app: English.
PS
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein.
XX
XX Sequence 181 AA;
SQ

Query Match 98.5%; Score 950; DB 23; Length 181;
Best Local Similarity 100.0%; Pred. No. 4e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 MAGGCSONEYFDSLLHACIPCOLRCSNTPPLTCORRYCNASVYNSKGNAILMTGLGS 63
DB 1 MAGGCSONEYFDSLLHACIPCOLRCSNTPPLTCORRYCNASVYNSKGNAILMTGLGS 60
OY 64 LIISLAVFVLMFLRKISSEPLKDEFFKNTGSGILGMANIDLEKSRGDEITLPRGLETTY 123
DB 61 LIISLAVFVLMFLRKISSEPLKDEFFKNTGSGILGMANIDLEKSRGDEITLPRGLETTY 120
OY 124 EECTCEDCIKSKRVSDHCPLPAMEGATVYTTKTYNDYCKSLPALSAFEIEKSISA 183
DB 121 EECTCEDCIKSKRVSDHCPLPAMEGATVYTTKTYNDYCKSLPALSAFEIEKSISA 180
OY 184 R 184
DB 181 R 181
RESULT 9
AAB60700
ID AAB60700 standard: protein: 157 AA.
XX
XX AAB60700;
AC
XX
XX 22-MAY-2001 (first entry)
DE
XX
XX Human BAFf receptor (BAFf-R) sequence encoded by a plasmid pJST535.
DE
XX
XX Human BAFf-R; BAFf receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200112812-A2.
PN
XX
XX 22-FEB-2001.
PD
XX
XX 16-AUG-2000; 2000WO-US22507.
PF
XX
XX 17-AUG-1999; 99US-0149378.
PR 11-FEB-2000; 2000US-0181684.
PR 18-FEB-2000; 2000US-0183536.
XX
XX (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
PI
XX
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
PI Thompson J;
DR WPI; 2001-202866/20.
DR N-PSDB; AAF60000.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFf-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFf-R
PT antibody homolog
XX
XX Example 1; Fig 3; 59pp: English.
PS
XX
XX The invention relates to the use of a BAFf receptor (BAFf-R, also known
CC as BCMA) protein, or a BAFf-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFf-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory

CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders. B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAFF-R protein sequence as encoded
 CC by plasmid pJ57535. However, this BAFF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.

XX Sequence 157 AA;

Query Match 74.6%; Score 719.5; DB 22; Length 157;
 Best Local Similarity 85.3%; Pred. No. 2.2e-69;
 Matches 157; Conservative 0; Mismatches 0; Indels 27; Gaps 9;

QY 1 MLOMACGCSQNEFYDLSLHACIPQLRCSNTPLTCQRCNMSVYNSVGTNAIIMTCL 60

DB 1 MLOMAG---ONEFYDLSLHACIPQLR---NTPPLTCQRCNMSVYNSVGTNAIIMTCL 51

QY 61 GLSLITSLAVFVLMFLRKISSEPLKDEFKNTSGLLGMANIDLEKSRGTDEIILPRGLE 120

DB 52 GLSLIITS---FVLMFLRKISSEPLK---NTSGLLGMANIDLEK---DEIILPRGLE 102

QY 121 YTVVECTCEDCIKSKRPVSDHCFPLPAMEGATIIIVTTKTNDYCKSLPALSATLEIKS 180

DB 103 YTVVECT---CIKSKRPVSDHCFPLP---EGATIIIVTTKTNDYCKS---ALSATLEIKS 153

QY 181 ISAR 184

DB 154 ISAR 157

RESULT 10

ID AAB08844 standard; peptide; 185 AA.

AC AAB08844;

DT 02-JAN-2001 (first entry)

DE Amino acid sequence of murine BCMA polypeptide.

XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;

KM anti-cell death gene; apoptosis; viral infection; inflammatory response;

KM rheumatoid arthritis; inflammatory bowel disease; septic shock.

OS Mus musculus.

XX Key

FT Domain

PN WO200050633-A1.

PD 31-AUG-2000.

PF 24-FEB-2000; 2000MO-US04925.

PR 24-FEB-1999; 99US-0121485.

XX (GEHO) GEN HOSPITAL CORP.

XX Seed B, Ting A;

PI WPI: 2000-558405/51.

DR Identifying a modulator of gene expression for drug designing, by

PT contacting a compound library with a cell expressing an anti-cell death

PT gene and reporter gene, and determining alteration in reporter gene

PS expression -

XX Claim 32; Fig 7B; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)-kB activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,
 CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing.

SQ Sequence 185 AA;

Query Match 59.3%; Score 572; DB 21; Length 185;
 Best Local Similarity 62.6%; Pred. No. 2.1e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MAGGCSQNEFYDLSLHACIPQLRCSNTPLTCQRCNMSVYNSVGTNAIIMTCLGSL 63

DB 1 MAGGCFSEFYDLSLHACIKRCHLRCSN--PPATCQPCDCPSVYNSVGTIVIMIFGLT 58

QY 64 LIISLAVFVLMFLRKISSEPLKDEKFN---TSGLLGMANIDLEKSRGTDEIILPRGL 119

DB 59 LVLSLAFITTSFLRKKNPALKDEPSPQLDGSALDKRADYELTIRAGDDRIFFRSL 118

QY 120 EYTVVECTCEDCIKSKRPVSDHCFPLPAMEGATIIIVTTKTNDYCK-SLPAL-SATFI 177

DB 119 EYTVVECTCEDCVKSKRPVSDHCFPLPAMEGATIIIVTTKTNDYCKSVPTALQSYGM 178

QY 178 EKSIAR 184

DB 179 EKPTHTR 185

RESULT 11

ID AAY71980 standard; Protein; 185 AA.

AC AAY71980;

DT 28-MAR-2001 (first entry)

DE Murine B cell maturation factor (BCMA) protein.

XX Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;

KM Tumour necrosis factor and ApoL-related Leucocyte expressed ligand 1;

KM therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KM systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

KM thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;

KM haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;

KM B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;

KM post-streptococcal glomerulonephritis; polyarteritis nodosa.

XX Mus musculus.

PN WO200068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12266.
 XX
 PR 06-MAY-1999; 99US-0132892.
 XX
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NAME-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Shu HS;
 XX
 DR WPI: 2001-016094/02.
 DR N-PSDB; AAD02130.
 XX
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 PS Claim 37; Page 107-108; 112pp; English.
 XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present invention is a murine B cell maturation factor (BCMA).
 CC BCMA is the receptor for TALL-1 protein.
 CC
 XX Sequence 185 AA;
 SO
 Query Match 59.3%; Score 572; DB 22; Length 185;
 Best Local Similarity 62.6%; Pred. No. 2,1e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
 QY 4 MAGGCSQNEYFDSLLHACIPQCLGSSNTPLTCORICMASVNSVKTNAIILMTCLGLS 63
 DB 1 MAQCCFSEYFDSLLHACKPCHLRCSN--PPATCOPYCDPSVTSVKGTYVLMIFGLT 58
 QY 64 LIISLAVFLMLFLLRKISSEPLKDFKN---TSGILGMANIDLEKSRGDEIILPRGL 119
 DB 59 LVLSLAFFTISFLLRKKNPEALKDEPQSPGQLDQSAQIDKADTETLRIRAGDDRIFFPSL 118
 QY 120 EYVEECTCEDCISKRPVSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 DB 119 EYVEECTCEDCVKSKPGSDHFFPLPAMEGATILVTTKTGDKSSVPTALQSVWGM 178
 QY 178 EKXSISAR 184
 DB 179 EKPTHTR 185
 RESULT 12
 ID AAE15490 standard; Protein; 185 AA.
 AC AAE15490;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse B cell maturation (BCMA) protein.

XX
 KW Mouse; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Mus sp.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 XX
 DR WPI: 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure: Fig 11; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein.
 XX
 SO Sequence 185 AA;
 Query Match 59.3%; Score 572; DB 22; Length 185;
 Best Local Similarity 62.6%; Pred. No. 2,1e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
 QY 4 MAGGCSQNEYFDSLLHACIPQCLGSSNTPLTCORICMASVNSVKTNAIILMTCLGLS 63
 DB 1 MAQCCFSEYFDSLLHACKPCHLRCSN--PPATCOPYCDPSVTSVKGTYVLMIFGLT 58
 QY 64 LIISLAVFLMLFLLRKISSEPLKDFKN---TSGILGMANIDLEKSRGDEIILPRGL 119
 DB 59 LVLSLAFFTISFLLRKKNPEALKDEPQSPGQLDQSAQIDKADTETLRIRAGDDRIFFPSL 118
 QY 120 EYVEECTCEDCISKRPVSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 DB 119 EYVEECTCEDCVKSKPGSDHFFPLPAMEGATILVTTKTGDKSSVPTALQSVWGM 178

OY 178 EKSISAR 184
 11 -
 Db 179 EKPTHTR 185

RESULT 13

AAE15501

ID AAE15501 standard; peptide; 58 AA.

AC AAE15501;

DT 12-MAR-2002 (first entry)

DE Human B cell maturation protein cysteine rich extracellular region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US15567.

XX PR 12-MAY-2000; 2000US-204039P.

XX PR 27-JUN-2000; 2000US-214591P.

XX PR 14-MAY-2001; 2001US-0214591.

XX PA (AMGE-) AMGEN INC.

XX PI Thell LE, Yu G;

XX DR WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand

XX Disclosure; Fig 13; 94pp: English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region.

XX Sequence 58 AA:

Query Match 33.5%; Score 323; DB 23; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3e-27;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSQNEYFDLHACIPQQLRCSSNPPPLTCORNCASVSNKYGTNAIIIMTCIGSLI 65

Db 1 CSQNEYFDLHACIPQQLRCSSNPPPLTCORNCASVSNKYGTNAIIIMTCIGSLI 58

RESULT 14

AAE15491

ID AAE15491 standard; Protein; 117 AA.

AC AAE15491;

DT 12-MAR-2002 (first entry)

DE Human-murine B cell maturation protein (BCMA) consensus sequence.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.

XX ChimERIC - Homo sapiens.

XX ChimERIC - Mus sp.

XX WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US15567.

XX PR 12-MAY-2000; 2000US-204039P.

XX PR 27-JUN-2000; 2000US-214591P.

XX PR 14-MAY-2001; 2001US-0214591.

XX PA (AMGE-) AMGEN INC.

XX PI Thell LE, Yu G;

XX DR WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand

XX Disclosure; Fig 11; 94pp: English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human-murine B cell maturation protein (BCMA) consensus sequence.

XX Sequence 117 AA:

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:57:01 ; Search time 25.2704 Seconds
(without alignments)
214.236 Million cell updates/sec

Title: US-09-848-271-2

Perfect score: 964

Sequence: 1 MLQAGGCSQNEFYDSLHA.....CKSLPALSTATEIKSISAR 184

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79.5	8.2	1009	2	US-08-357-642A-1
2	79.5	8.2	1009	2	US-08-460-626-1
3	78.5	8.1	293	2	US-08-810-572A-2
4	78.5	8.1	293	4	US-09-290-333-2
5	76	7.9	744	1	US-08-179-481-2
6	75	7.8	857	1	US-07-717-331E-2
7	70.5	7.3	154	4	US-09-232-160-18
8	69.5	7.2	166	2	US-08-810-572A-6
9	69.5	7.2	166	4	US-09-290-333-6
10	69.5	7.2	1180	4	US-08-660-148-2
11	69.5	7.2	1212	4	US-08-660-148-5
12	69.5	7.2	1706	2	US-08-459-568-2
13	69.5	7.2	1706	2	US-08-399-411-2
14	69.5	7.2	1706	3	US-08-516-859A-2
15	69.5	7.2	1706	4	US-09-586-472-2
16	69.5	7.2	1706	4	US-09-528-706-2
17	69.5	7.2	2496	4	US-09-125-028-2
18	69.5	7.2	2958	4	US-08-894-344C-2
19	69	7.2	324	2	US-08-579-940-7
20	69	7.2	445	1	US-08-353-400-33
21	69	7.2	447	6	5455030-1
22	69	7.2	464	1	US-08-353-400-36
23	69	7.2	599	1	US-08-442-542-18
24	69	7.2	599	3	US-08-765-469-18
25	68.5	7.1	295	3	US-08-651-136C-8
26	68.5	7.1	295	4	US-09-229-911A-8
27	68.5	7.1	877	1	US-08-072-574-12

28	68.5	7.1	877	1	US-08-486-270-12
29	68.5	7.1	877	3	US-08-367-264-12
30	68.5	7.1	877	4	US-09-153-757-12
31	68.5	7.1	1180	1	US-08-072-574-8
32	68.5	7.1	1180	1	US-08-486-270-8
33	68.5	7.1	1180	3	US-08-367-264-8
34	68.5	7.1	1180	4	US-09-153-757-8
35	68.5	7.1	1212	1	US-08-072-574-10
36	68.5	7.1	1212	1	US-08-486-270-10
37	68.5	7.1	1212	3	US-08-367-264-10
38	68.5	7.1	1212	4	US-09-153-757-10
39	68	7.1	317	2	US-08-466-337A-18
40	68	7.1	317	2	US-08-475-359-18
41	68	7.1	317	3	US-08-465-887A-18
42	67.5	7.0	178	1	US-08-825-891-1
43	67.5	7.0	799	1	US-08-188-228-42
44	67.5	7.0	799	1	US-08-332-638-42
45	67	7.0	182	3	US-09-045-632-29

ALIGNMENTS

RESULT 1
US-08-357-642A-1
; Sequence 1, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: PYK2 RELATED PRODUCTS
; NUMBER OF INVENTIONS: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-357-642A-1
Query Match 8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 2.5;

Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

OY 88 EFKNNGSLGGMANIDLEKSR-----TGDEILIRGLETYVEECTCEDCISKRPV 138
Db 249 KFFNT---LAGFANIDQETRYCELLQGMNITVDLVIGPKGIRHOLTSQDAKPTCLAEFRQI 305

OY 139 DSDHCFPLPAMEGATIL 156
Db 306 RSTRICPL---EKGAVL 320

RESULT 2
US-08-460-626-1
; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-460-626-1

Query Match 8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 2.5;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

OY 88 EFKNNGSLGGMANIDLEKSR-----TGDEILIRGLETYVEECTCEDCISKRPV 138
Db 249 KFFNT---LAGFANIDQETRYCELLQGMNITVDLVIGPKGIRHOLTSQDAKPTCLAEFRQI 305

OY 139 DSDHCFPLPAMEGATIL 156
Db 306 RSTRICPL---EKGAVL 320

RESULT 3

US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-1684
; TELEFAX: 201-487-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-2

Query Match 8.1%; Score 78.5; DB 2; Length 293;
Best Local Similarity 19.9%; Pred. No. 0.56;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

OY 8 CSQNEVFDLHACIPQCRSSNTPPLTCORVCNASVTNSVKGT--NALIMTGLISLI 65
Db 34 CPEQYWDPLGTCTMCKTICNHOS-ORTCAATCRSLCKRQCKFYDHLRDTSCASI 92

OY 66 I-----SLAVFVLMFL-----LKRISSEPLKDEKNTGSLQGMANIDLEKS---- 107
Db 93 CGQHPKOCAYFCENKILSPVNLPELRRORSCEVENNSDSNGR-YGLERHGSASPALP 151

OY 108 ---RTGDEILIRPG-----LETVVECTCEDCISKRP-----KVD 139
Db 152 GLKISADQVALVYSTGLCLCAVLCFLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209

OY 140 SDHCFPLPAMEGATILVTTKTNDYC 165
Db 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 4
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:

```

APPLICANT: Bram, Richard J.
            von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
                    CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                    THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
            Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290.333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match      8.1%; Score 78.5; DB 4; Length 293;
Best Local Similarity 19.9%; Pred. No. 0.56;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY      8 CSQNEYRDSLLHACIPQCLKSSNTPPLTCORVCNASTYNSVKGTT--NAIIWTLGSLI 65
      1 : : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
Db      34 CPEDQYMDPLGLTGMSCKTCIKNHQS-QRTCAAFGRSLSCRRGCKFYDHLIRDISCASI 92
QY      66 I-----SLAVVLMFL-----LKRISSEPLKDEKKNQSGILGMANIDLKRS----- 107
Db      93 CGGHPKQCAFCFCEKNLSPVNLPPELRLRORSGEVENNSDNGR-YQGLEHSGEASPALP 151
QY      108 ---RTGDEIILPRG-----LETVVECTGCEDCIKSRP-----KVD 139
Db      152 GLKISADQVALVAVTSLGICLCALVLCGFLVAVACFLKKRGDCSCQP--RSNPRPSPAKSS 209
QY      140 SDHCFFPLPAMEGATILVTTKTDNYC 165
      11 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
Db      210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 5
US-08-179-481-2
; Sequence 2, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARRAWAY, KERMIT L.
; APPLICANT: CARROTHERS CARRAWAY, CORALIE A.
; APPLICANT: FREGIEN, NEVIS L.

```

```

? TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
? NUMBER OF SEQUENCES: 125
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
? STREET: 1100 NEW YORK AVENUE, N.W.
? CITY: WASHINGTON
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005-3918
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/179,481
? FILING DATE: 28-DEC-1993
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/922,521
? FILING DATE: 30-JUL-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: KOKUBIS, PAUL N.
? REGISTRATION NUMBER: 16,773
? REFERENCE/DOCKET NUMBER: 200702/DW92-08CIP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 861-3000
? TELEFAX: (202) 822-0944
? TELEX: 6714627 CUSH
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 744 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-179-481-2

Query Match      7.9%; Score 76; DB 1; Length 744;
Best Local Similarity 22.1%; Pred. No. 4.2;
Matches 34; Conservative 29; Mismatches 57; Indels 34; Gaps 6,

OY   4 MAGCCSQNEYRDSLHACIFPCOLRCSSNTPPLTCORYC-----NASVTSNAKCT 52
    :|:|:|:|:|:| | | | | | | | | | | | | | | | | | | | | | |
Db   49 LEGRTAQCDSNATNFIAFAAQYNNTSLKSPIYVMFLPNDIRVHNNOVAFTSPT 108
OY   53 NATLMTGLGSLI-----ISLAFFVLMPILRKITSSEPLEDEFKNTSGLLG 98
    :|:|:|:|:|:| | | | | | | | | | | | | | | | | | | | | | |
Db   109 EDLEVFNATGVLLIONGQSVSNFEGVTIVTIALSNITLHAASS--LSFEYRNHTKGLLG 166
OY   99 MANIDLEKSRFGDELIILPRGLETVVEECTCEDCI 132
    :|:|:| | | | | | | | | | | | | | | | | | | | | | |
Db   167 VMNDPE-----DDFRMPNG--STIPSNSTSETL 193

RESULT 6
US-07-717-331F-2
: Sequence 2, Application us/07717331F
: Patent No. 5484905
GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yanwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
```

COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-717-331F-2

Query Match 7.8%; Score 75; DB 1; Length 857;
Best Local Similarity 17.6%; Pred. No. 6.6;
Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

QY 24 COLRCSNTPPLTCORCNASVTNSVKGNAIILMT-----58
DB 380 CKKRISD---CNCYAFANADIRNG--GSGCYIWTRELEDIRNVTADIDGODLVRLAA 434
QY 59 -----CGLSLIISLAVFLMFLRKISSEPLKDEKFTGSGGLGMANIDLEK 106
DB 435 ADIAKRNASGKIISLTVGVSULLIMECL-----WKRRKAKAKASISANTQKNO 487
QY 107 SRTDEILLRGLRGLTVECTCECIRKRPVDSNCF-----PIPAEEGATILVTTKT 161
DB 488 NLPNHEVYL-----SSKREFSGEYKFELELPIEME---TVVKATEN 527
QY 162 NDYCKSL 168
DB 528 FSSCNKL 534

RESULT 7
US-09-232-160-18
Sequence 18, Application US/09232160
Patent No. 6368794
GENERAL INFORMATION:
APPLICANT: Steve Daniel
APPLICANT: James Gilmore
APPLICANT: Susan G. Stuart
APPLICANT: Laura Stuve
TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
FILE REFERENCE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1299627
US-09-232-160-18

Query Match 7.3%; Score 70.5; DB 4; Length 154;
Best Local Similarity 25.2%; Pred. No. 1.9;
Matches 30; Conservative 16; Mismatches 52; Indels 21; Gaps 6;

QY 13 YFSLSLHAC-IPQLRCSNTPPLTCORCNASVTNSVKGNAIILMTCLG-----LSLIIIS 67
DB 23 YADDCIAOCCGCKDCKSYCCDGTPTCCSY--AVIGNILST-ALAGIVEIIVIMGVIA 79

QY 68 LAVFLMLLRKISSEPLKDEKFTGSGGLGMANIDLEKSRGTDEIILRGLRGLTVEEC 126
DB 80 IAIICMCM-----KNHRATRVGILRTHINTVSSYICPP---PYGDHEMEYC 125

RESULT 8
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 7.2%; Score 69.5; DB 2; Length 166;
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

QY 8 CSQNEFDSLHAC-IPQLRCSNTPPLTCORCNASVTNSVKGNAIILMTCLGSLI 65
DB 34 CPBQYWDPLGLTCMSCKTICNHOS-ORTCAAFCRSLSCRKEDGKFYDHLRDCISCASI 92

RESULT 9
US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 7.2%; Score 69.5; DB 4; Length 166;
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

QY 8 CSONEYFDSLHACIPQRCSSNTPPLTCQRYCNASTVNSVKGT--NAIIMTCLGLSLI 65
DB 34 CPEQIWDPLGTCKMCKTCINHG--QRTCAFCRSLCRKQKPYDHLRDCISCASI 92

RESULT 10
US-08-660-148-2
Sequence 2, Application US/08660148
Patent No. 6211353
GENERAL INFORMATION:
APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Snyder, Yvonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-148-2

Query Match 7.2%; Score 69.5; DB 4; Length 1180;
Best Local Similarity 24.6%; Pred. No. 46;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSONEYFDSLHACIPQRCSSNTPPLTCQRYCNASTVNSVKGN-----AIIMTCLG 61
DB 537 CKENEYVDE--YTCACQLG--SWPTDILT---GCDLIPVOYLKWDDEPIAAVVFACLG 590
QY 62 LSLIISLAVFVLMFLR-----KISEPLKDFKNTGSLGLMANIDLEKSRTEIILP 116
DB 591 --LWATLFVTVFIIIRDPVVKSSREL-----YIIL 622
QY 117 RLEYTVEEC---TCEDCIKSKPYVDSHCF-----PLPAMECATILVTTKTN----- 162
DB 623 AGI-----CLGYLCFFCLIAKPK--QIYCYLQIGIGLSPAMSYSAIV---TKTWRIAR 671
QY 163 -----DYCKSLPALSLA 174
DB 672 ILAGSKKIKITKPKRPMISA 690

RESULT 11
US-08-660-148-5
Sequence 5, Application US/08660148
Patent No. 6211353
GENERAL INFORMATION:
APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Snyder, Yvonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-148-5

Query Match 7.2%; Score 69.5; DB 4; Length 1212;
Best Local Similarity 24.6%; Pred. No. 47;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSQNEY-PDSLHACIPCOLRCSNTPPLTCORCNASVTSVKGTN-----AIIWTCIG 61
DB 537 CKENYVDE--YTCKACQLG-SWPTDILT---GCDLIPVQYLRMGDEPIAAVAVFACLG 590
QY 62 LSLIISLAVFVLMFLR-----KISSEPLKDEPKNTGSGLLGMANIDLEKSRGTDEIILP 116
DB 591 --LATLEFVTVFIIYRDTPVVKKSSRELQ-----YIIL 622
QY 117 RGLGYVEEC---TCEDCIKSKPKVDSHCF-----PLPAMEGATILVTTKTN----- 162
DB 623 AGI-----CIGYCTFELIKPK--QIYCYLQIGTIGLSPMYSALV---TKNRIRAR 671
QY 163 -----DYCKSLPALSA 174
DB 672 ILAGSKKIKCTKKRPFMSA 690

RESULT 12

US-08-459-568-2

Sequence 2, Application US/08459568

Patent No. 5811304

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,568

FILING DATE: 02-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,411

FILING DATE: 06-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1264

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-568-2

Query Match 7.2%; Score 69.5; DB 2; Length 1706;
Best Local Similarity 21.7%; Pred. No. 77;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

QY 34 PLTCORCNASVTSVKGNAILMTCTGLISLISLAVFVLMFLRKISSEPLKDEPKNTG 93
DB 598 PVTVE-----ITONIKSTQV-----SYHDDLKDSPTST- 626
QY 94 SGLLGMANIDLEKSRGTDEIILPRLGLEYVECTCEDCIKSKP-----KYSDHCFPLP 147
DB 627 -----NCESKRRTPAPVLPKIKETEDSDTAPSCSLPLSLISIAEVSRH----- 674
QY 148 AMEGATILVTTKTNDYCK-----SLPALSAETEHEK 179
DB 675 -KENG-VYLSKKLQLLQTDKLTLPAGFSAAETPK 708

RESULT 13

US-08-399-411-2

Sequence 2, Application US/08399411

Patent No. 5831008

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/399,411

FILING DATE: 06-MAR-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1264

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1706 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-399-411-2

Query Match 7.2%; Score 69.5; DB 2; Length 1706;
Best Local Similarity 21.7%; Pred. No. 77;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

QY 34 PLTCORCNASVTSVKGNAILMTCTGLISLISLAVFVLMFLRKISSEPLKDEPKNTG 93
DB 598 PVTVE-----ITONIKSTQV-----SYHDDLKDSPTST- 626
QY 94 SGLLGMANIDLEKSRGTDEIILPRLGLEYVECTCEDCIKSKP-----KYSDHCFPLP 147

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Db 627 -----NCESKRRRTASPPPLPKIKETEDSDTAAPGCSLSPLSTIAEYVSH----- 674
Qy 148 AMEGATILVTYTKNDYCK-----SLPALSAITEIK 179
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Db 675 -KEKG--VYLSKRLQLQTDKLTLPAGFSMAAIPK 708

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RESULT 14

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US-08-516-859A-2
: Sequence 2, Application US/08516859A
: Patent No. 6069231
: GENERAL INFORMATION:
: APPLICANT: Huang, Shi
: TITLE OF INVENTION: Retinoblastoma Protein - Interacting
: TITLE OF INVENTION: Zinc Finger Proteins
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/516,859A
: FILING DATE: 18-AUG-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: PRIOR APPLICATION NUMBER: US 08/399,411
: FILING DATE: 06-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/292,683
: FILING DATE: 18-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-LJ 1776
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1706 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-516-859A-2

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	Query Match	7.2%	Score 69.5:	D8 3,	Length 1706:	
	Best Local Similarity	21.7%:	Pred. NO. 77:			
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	: : : : : :			:	:	:
	I : I : I : I : I :			:	:	:
Db	598 PVTVE-----ITQNIKNQV-----SYVDLLKDKSSSF-	626				
OY	94 SGLLOMANIDLEKSRIGDEIILPRLELYVEECTEDCIKSP-----KVDSRHCFPIIP	147				
	: : : : : :			:	:	:
	I : I : I : I : I :			:	:	:
Db	627 -----NCESKKRRRTASPVLPIKTKTESDSTAPSCLSPLISTAEVVSFH-----	674				
OY	148 AMEGATIIIVTTKTNDYCK-----SLPALSNTEIEK	179				
	: : : : : :			:	:	:
	I : I : I : I : I :			:	:	:
Db	675 -KEKG-VYLSSKLKOLLQTDOKTLPLPAFSAAEIIPK	708				

RESULT 15

US-09-586-472-2
; Sequence 2, Application US/09586472

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Patent NO. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
                                Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-586-472-2

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Query Match	7.2%	Score 69.5:	DB 4,	Length 1706:
Best Local Similarity	21.7%	Pred No. 77:		
Matches 34:	Conservative 22:	Mismatches 44:	Indels 57:	Gaps 7.
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Db	598	PATVE-----ITQNIKQV-----SVTDLLKDKSSST-	626	
QY	94	SGLLGMANIDLEKSRFGDEIILPRGLETVVEECTCEDCIKSP-----KVDSDHCFLPL	147	
Db	627	-----NCESKRRRTASPVLPKIKTETESDSTPASCPLSLISTAEVVFH----	674	
QY	148	AMEGATILVTKTNDYCK-----SLPALSTTELEK	179	
Db	675	-KEKG-VYLLSKKOLLQTDKLLPAPAFSAAEIIP	708	

Search completed: November 12, 2002, 17:01:40
Job time : 28.2704 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 17:00:26 : Search time 14.2146 Seconds
(without alignments)
186.640 Million cell updates/sec

Title: US-09-848-271-2

Perfect score: 964
Sequence: 1 MLAGGCGSCNNEYFDSLHA.....CKSLPALSAIEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PCRT_NEM_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubppaa/US10_NEM_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US60_NEM_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	950	98.5	181	10	US-09-854-864-5
2	572	59.3	185	10	US-09-854-864-11
3	323	33.5	58	10	US-09-854-864-21
4	311.5	32.3	117	10	US-09-854-864-12
5	286	29.7	283	10	US-09-854-864-9
6	284	29.5	51	10	US-09-854-864-6
7	201	20.9	34	10	US-09-854-864-7
8	201	20.9	81	10	US-09-854-864-13
9	187	19.4	281	10	US-09-854-864-10
10	104	10.8	21	10	US-09-854-864-8
11	79.5	8.2	293	9	US-09-779-050A-42
12	79.5	8.2	1009	8	US-08-987-689A-2
13	78.5	8.1	293	10	US-09-879-919-22
14	78.5	8.1	293	10	US-09-854-864-14
15	78.5	8.1	293	10	US-09-961-376-2
16	78	8.1	291	9	US-09-779-050A-43
17	70.5	7.3	397	9	US-09-854-864-18
18	70.5	7.3	1203	12	US-10-027-923-5
19	70	7.3	180	10	US-09-780-717-11

20	70	7.3	182	10	US-09-780-717-44	Sequence 44, Appl
21	70	7.3	836	10	US-09-925-301-1088	Sequence 1088, Ap
22	69.5	7.2	59	10	US-09-854-864-20	Sequence 20, Appl
23	69.5	7.2	166	10	US-09-854-864-15	Sequence 15, Appl
24	69.5	7.2	1212	12	US-10-027-923-4	Sequence 4, Appl1
25	69	7.2	324	10	US-09-797-481-7	Sequence 7, Appl1
26	69	7.2	772	10	US-09-815-837-74	Sequence 74, Appl
27	69	7.2	774	10	US-09-815-837-72	Sequence 72, Appl
28	68.5	7.1	305	10	US-09-771-730-119	Sequence 119, App
29	67.5	7.0	37	9	US-09-779-050A-45	Sequence 45, Appl
30	67.5	7.0	664	10	US-09-780-525-2	Sequence 2, Appl1
31	67	7.0	320	10	US-09-797-481-8	Sequence 8, Appl1
32	67	7.0	1113	10	US-09-836-470B-3	Sequence 3, Appl1
33	66.5	6.9	67	10	US-09-854-864-16	Sequence 16, Appl
34	66	6.8	317	9	US-09-844-988-1	Sequence 1, Appl1
35	66	6.8	317	10	US-09-844-908-1	Sequence 1, Appl1
36	66	6.8	376	10	US-09-735-787-4	Sequence 4, Appl1
37	65.5	6.8	728	10	US-09-908-322-2	Sequence 2, Appl1
38	65.5	6.8	798	12	US-10-078-929-192	Sequence 192, App
39	65.5	6.8	3034	10	US-09-737-149-25	Sequence 25, Appl
40	65.5	6.8	3034	10	US-09-737-149-30	Sequence 30, Appl
41	65	6.7	386	12	US-10-039-785-4	Sequence 4, Appl1
42	65	6.7	386	12	US-10-105-929-6	Sequence 6, Appl1
43	64.5	6.7	195	10	US-09-005-243-44	Sequence 44, Appl
44	64.5	6.7	195	10	US-09-224-683-44	Sequence 44, Appl
45	64.5	6.7	418	9	US-09-886-429-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EVDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGE-3, AND TAC1
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match          98.5%; Score 950; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 MLAGGCGSCNNEYFDSLHACIPCOLRCSSNPPYTCORCYNASTYNSVKGNNATILMTCLIGS 63

DB 1 MLAGGCGSCNNEYFDSLHACIPCOLRCSSNPPYTCORCYNASTYNSVKGNNATILMTCLIGS 60

QY 64 LIISLAVFLMFLRKRISEPLKDEFKNTGSLGMANIDLEKSRFGDEIILPRGLETVV 123

DB 61 LIISLAVFLMFLRKRISEPLKDEFKNTGSLGMANIDLEKSRFGDEIILPRGLETVV 120

QY 124 EECTCEDCKSRPKYDSHCFPLPAMEGATITLVTTKINDYKSLPALSAIEIKSISA 183

DB 121 EECTCEDCKSRPKYDSHCFPLPAMEGATITLVTTKINDYKSLPALSAIEIKSISA 180

QY 184 R 184

Db 181 R 181

RESULT 2
US-09-854-864-11; Sequence 11, Application US/09854864
; Patent No. US20020081296A1

GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: BLYS/AGP-3, AND TACI

; CURRENT APPLICATION NUMBER: US/09/854,864

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Murine

US-09-854-864-11

Query Match

59.3%; Score 572; DB 10; Length 185;

Best Local Similarity 62.6%; Pred. No. 4,8e-51;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

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Db 1 MDDCHSEFFDLSLHACIPCOLRCSSNTPPLTCORCMASVTNSVKGCTNAILMTCLGLS 58

QY 64 LIISLAVFLMLFKRKISSEPLKDEFEKN---TGSGILGMANIDLEKSRGTDEIILPRG 119

Db 59 LVLSLALFTISFLRKMPALKEPQSGQDLSQDLKADIELTRIRAGDDRIRPRSL 118

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Db 119 EYVEEECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSSVPTALQSVGM 178

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Db 179 EKEPTMR 185

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Db 179 EKEPTMR 185

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Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSONEFYDLSLHACIPCOLRCSSNTPPLTCORCMASVTNSVKGCTNAILMTCLGLSLI 58

RESULT 4
US-09-854-864-12; Sequence 12, Application US/09854864
; Patent No. US20020081296A1

GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: BLYS/AGP-3, AND TACI

; CURRENT APPLICATION NUMBER: US/09/854,864

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 117

; TYPE: PRT

; ORGANISM: human-murine Consensus

US-09-854-864-12

Query Match

32.3%; Score 311.5; DB 10; Length 117;

Best Local Similarity 61.5%; Pred. No. 7.5e-25;

Matches 96; Conservative 4; Mismatches 7; Indels 49; Gaps 19;

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Db 2 AOEYFDSLHACIPCOLRCSSNTPPLTCORCMASVTNSVKGCTNAILMTCLGLSLI 43

QY 69 AVEVLMFLMKRKISSEPLKDEFEKN---TGSGILGMANIDLEKSRGTDEIILPRGLETVVECTG 128

Db 44 A-----FELLRK-----ELKDE-----GSLAL-----RGD---IPR-LETVVECTG 76

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Db 77 EDC-KSKPK-DSDH-FPLPAMEGATILVTTKT-DY 108

QY 129 EDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDY 164

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Query Match          29.7%; Score 286; DB 10; Length 283;
Best Local Similarity 37.6%; Pred. No. 8.8e-22;
Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;

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DB 1 MAGCCSONEYFDSLHACIPQCLRCSSNTPPLTCORCYNASVYNSVKGTA 51
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OY 64 LIISLAVFVIMFLIRKISSPLKDEFKNTGSG-----LLGMANIDLEKSRIG 110
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DB 85 DTLMIKRTPEVT---CVYVDVSHEDPEVKRNMYVDGVEVHNATKREEDYNSTRYVS 141
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OY 157 VTKRTNDY-----CKSLPALSAFEIEKSSIS 182
    |||::|||::|||::|||::|||::|||::|||::|||::|||
DB 142 LTVLIHODWLNKKEYCKCKVSNKALPA-PIEKTI 173
    |||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 6
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match          29.5%; Score 284; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MAGCCSONEYFDSLHACIPQCLRCSSNTPPLTCORCYNASVYNSVKGTA 54
    |||||||||||||||||||||||||||||||||||||||||||||||
DB 1 MAGCCSONEYFDSLHACIPQCLRCSSNTPPLTCORCYNASVYNSVKGTA 51
    |||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7

Query Match          19.4%; Score 187; DB 10; Length 281;
Best Local Similarity 29.8%; Pred. No. 9.8e-12;

; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match          20.9%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCORC 41
    |||||||||||||||||||||||||||||||||||||||||||||
DB 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCORC 34
    |||||||||||||||||||||||||||||||||||||||||||||

RESULT 8
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match          20.9%; Score 201; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 7.8e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCORC 41
    |||||||||||||||||||||||||||||||||||||||||||||
DB 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCORC 34
    |||||||||||||||||||||||||||||||||||||||||||||

RESULT 9
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
```


Db 93 CGHPKOCATFCENKLNLPVNLPPELRRQRSGEVENNSDNGR-YOGLHRGSEASPALP 151
Qy 108 ---RTGDEIILPRG-----LEYTVEECTCEDCIKSKP-----KVD 139
Db 152 GLKLSADQVALVYSTIGICLCALVLCFLVAVACFLKKRGDPCSCOP--RSRPRQSPAKSS 209
Qy 140 SDHCPLPLAMEGATILVTTKTNDYC 165
Db 210 QDH-----AMEGSPVSTSPPEVETC 230

Search completed: November 12, 2002, 17:09:11
Job time : 15.2146 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:36 : Search time 28.4292 Seconds
(Without alignments)
622.203 Million cell updates/sec

Title: US-09-848-271-2

Perfect score: 964
Sequence: 1 MLOMAGQCSQNEFYFDSLHNA.....CKSLPALATSEIETKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	964	100.0	184	2 S43486	B-cell maturation
2	88.5	9.2	217	2 C97344	amino acid ABC tra
3	86.5	9.0	858	2 T08881	prominin - mouse
4	83.5	8.7	1998	2 T13009	hypothetical prote
5	82	8.5	1009	2 A57434	protein-tyrosine k
6	81.5	8.5	2233	2 T28669	surface protein 51
7	81	8.4	773	2 D89010	protein R08F11.7
8	79.5	8.2	1009	2 S60248	protein-tyrosine k
9	78.5	8.2	1299	2 T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	2 D64469	potassium channel
11	78	8.0	841	2 JC5894	Killer cell inhibi
12	77.5	8.0	738	2 D86345	hypothetical prote
13	77.5	8.0	968	2 T01733	hypothetical prote
14	77	8.0	522	2 T45824	hypothetical prote
15	77	8.0	539	2 F72288	methyl-accepting c
16	76.5	7.9	357	2 T21152	hypothetical prote
17	76.5	7.9	1404	2 T19277	hypothetical prote
18	76	7.9	744	2 A43353	asclites stialoglyc
19	76	7.9	748	2 T47250	complex I interned
20	75.5	7.8	638	2 T41478	probable transcrip
21	75	7.8	450	2 B97297	hydrogenase chain
22	75	7.8	857	1 A41369	S-receptor kinase
23	74.5	7.7	384	2 S45592	ERD1 protein - yea
24	74.5	7.7	1101	2 T16840	hypothetical prote
25	74	7.7	377	2 JC7535	chitinase (EC 3.2.
26	73.5	7.6	307	2 B95039	membrane protein
27	73.5	7.6	307	2 A97967	conserved hypotet
28	73	7.6	304	2 A89882	hypothetical prote
29	73	7.6	679	2 B96599	protein F20N2.12

30	73	7.6	733	1 A46373	probable serine/th
31	72.5	7.5	243	2 T31144	hypothetical prote
32	72.5	7.5	408	2 B84518	hypothetical prote
33	72	7.5	416	2 S75097	hypothetical prote
34	72	7.5	855	2 T10665	hypothetical prote
35	71.5	7.4	105	2 T10350	hypothetical prote
36	71.5	7.4	627	2 B71709	hypothetical prote
37	71	7.4	227	2 F72334	conserved hypotet
38	71	7.4	414	2 G71331	probable cell divi
39	71	7.4	473	2 AF1207	ABC transporters
40	71	7.4	480	2 G88690	protein F41H10.1
41	71	7.4	500	2 T10543	hypothetical prote
42	71	7.4	660	2 T02768	spike glycoprotein
43	70.5	7.3	188	2 H82933	hypothetical prote
44	70.5	7.3	412	2 T24023	hypothetical prote
45	70.5	7.3	424	2 T14525	S-locus-specific g

ALIGNMENTS

RESULT 1

S43486

B-cell maturation factor - human

N:Alternate names: BCM protein; BCMA protein; BEL protein

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence,revision 27-Jan-1995 #text,change 21-Jul-2000

C:Accession: S43486; S31208; S36651

R:Laabl, Y.; Gras, M.P.; Brown, J.C.; Berger, R.; Larsen, C.J.; Tsap, A.

Nucleic Acids Res. 22, 1147-1154, 1994

A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bl

A:Reference number: S43486; MUID:94218235; PMID:8165126

A:Accession: S43486

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-184 <LAA>

A:Cross-references: EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471245

R:Laabl, Y.; Gras, M.P.; Carbonnel, F.; Brown, J.C.; Berger, R.; Larsen, C.J.; Tsap

EMBO J. 11, 3897-3904, 1992

A:Title: A new gene, BCM, on chromosome 16 is fused to the Interleukin 2 gene by a t

A:Reference number: S31208; MUID:93010984; PMID:1396583

A:Accession: S31208

A:Molecule type: mRNA

A:Residues: 1-184 <LAA>

A:Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:929408

A:Accession: S36651

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 4-184 <LAA3>

A:Cross-references: EMBL:Z14955

C:Genetics:

A:Gene: GDB:BCMA

A:Cross-references: GDB:135977; OMIM:109545

A:Map position: 16p13.1-16p13.1

A:Introns: 44/1; 93/1

C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 964; DB 2; Length 184;

Best local similarity 100.0%; Pred. No. 5.6e-81;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MLOMAGQCSQNEFYFDSLHACIPCOLRCSSNTPPLTCORVCNASVTNSVKGTNATLWCL	60
DB	1	MLOMAGQCSQNEFYFDSLHACIPCOLRCSSNTPPLTCORVCNASVTNSVKGTNATLWCL	60
OY	61	GLSLTISLAVYLMFLRKISSEPLKDFKNTGSLGTMANIDLEKSRGTGEIILPRGLE	120
DB	61	GLSLTISLAVYLMFLRKISSEPLKDFKNTGSLGTMANIDLEKSRGTGEIILPRGLE	120
OY	121	VTVEECTCEDCICKSPKVDSDHCFPLPAMEEGATILVTTKINDYKSLPALATSEIERS	180
DB	121	VTVEECTCEDCICKSPKVDSDHCFPLPAMEEGATILVTTKINDYKSLPALATSEIERS	180

Oy 181 ISAR 184
Db 181 ISAR 184

RESULT 2

C97344
amino acid ABC transporter, permease component CAC3619 [Imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: C97344
R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: C97344
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81542.1; PID:g15026719; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3619
C:Superfamily: histidine permease protein M

Query Match 9.2%; Score 88.5; DB 2; Length 217;
Best Local Similarity 24.8%; Pred. No. 0.98;
Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

Oy 16 SLHACIFQCLGSCSNTPLTCORICNASV-----TNSVKGTNAI---LWTCUGL 62
Db 4 SLNVTIPLVLDGTRITLLTCSIIIGIITIAMFKTSVKVNLNGKFTYWLKGT 63
Oy 63 SLIISLAVFV--LMLFLRKISSEPLKDEF---KNTGS-----GLIGMANIDLEKSR 108
Db 64 PLLDLVYYVYGLPLPSDKLTWTPKKAAILGLSLNSGATIAETTGILAIIDNGCFEASK 123
Oy 109 -----TGDEIILPRGLETYVEEC-----TCEDCI-KSKPVVDSDH 142
Db 124 ALGLTGYGTMKRRIIPQAIRVIVPCGNEFIAMIKDTLSVITYMEELLRKQQLLVSSSG 183
Oy 143 CFPPLAMEGA--TLVTTKTNDYCKSLPAALSAFIEKIS 182
Db 184 DAVTPYLPAGIFLYLTITITGIFSK-----IEKIS 215

RESULT 3

T08881
promilin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08881
R:Weligmann, A.; Corbell, D.; Hellwig, A.; Huttner, W.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A:Title: Promilin, a novel microvilli-specific polytopic membrane protein of the apical
A:Reference number: 216512; MUID:98024147; PMID:9356465
A:Accession: T08881
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-858 <WEI>
A:Cross-references: EMBL:AF026269; NID:g2559003; PIDN:AA86715.1; PID:g2559004
A:Experimental source: kidney
C:Keywords: glycoprotein; membrane protein

Query Match 9.0%; Score 86.5; DB 2; Length 858;
Best Local Similarity 22.7%; Pred. No. 6;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

Oy 18 LHACIFQCLGSCSNTPLTCORICNASVNTNSVKTNAIIMTCLSLIISLAVFVLMFL 77
Db 117 LVGCFQCMCR-----CMK-CGGEHMOKQKNAFCKRCKGLSLVYICLMSGLIIT 167

Oy 78 RKISSEPLKDEFKNTGSGGLGMANIDLEKSRIGD-EIIL---PRGLETYVECTCE---- 129
Db 168 GFVANQOTRTRIKGTOK-----LAKSNFRDFOITLTPKQIDVVEQYOTNRKKA 218

Oy 130 ----DCIKS-----KKPVSDHCFPLPAMEGATILVTTK--TNDYCKSLPAAL-- 172
Db 219 FSDLDGTSVVGRIKIDLPKRV-----TPVEIEIKAMATAIKOTDALQNMSSLSKS 271

Oy 173 ---SATEIEKSISA 183
Db 272 IQDATQQLNTNLS 285

RESULT 4

T13009
hypothetical protein T24C20_80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Nov-1999
R:Choline, N.; Robert, C.; Brotlier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.;
submitted to the Protein Sequence Database, July 1999
A:Reference number: 217586
A:Accession: T13009
A:Molecule type: DNA
A:Residues: 1-1998 <CHO>
A:Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20_80
A:Experimental source: cultivar Columbia; BAC clone T24C20
C:Genetics:
A:Gene: ATSP:T24C20_80
A:Map position: 3
A:Insertions: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/

C:Superfamily: Arabidopsis thaliana hypothetical protein T24C20_80

Query Match 8.7%; Score 83.5; DB 2; Length 1998;
Best Local Similarity 29.4%; Pred. No. 27;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Oy 38 QRYCNASVTVNSVKTNAIIMTCLSLIISLAVFVLMFLRKISSEPLKD-EFKN--TGS 94
Db 1089 ERYCSA---NSALGTPSM---C-----SSRGPPQDSFEVNFSLGP 1122

Oy 95 GLIGMANIDLEKSRIGDEIILPRGLETYVEECTCDECIKSRP-----KVSDHCFPLPAM 149
Db 1123 SLVRLSLSDM--SRIGD-----RGTHFDEGSGCMGRSSAPAGLNTGWNIDMCGDI--M 1173

Oy 150 EECAT 155
Db 1174 DGGATI 1179

RESULT 5

A57434
protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat
N:Alternate names: cell adhesion kinase-beta
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 04-Feb-2000
C:Accession: A57434

R:Sasaki, H.; Nagura, K.; Ishino, M.; Tobioke, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A:Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-t
A:Reference number: A57434; MUID:95403356; PMID:7673154
A:Accession: A57434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1009 <SAS>

A:Cross-references: GB:D45854; NID:g1000679; PIDN:BA08290.1; PID:d1008885; PID:g1000
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: Arp; phosphotransferase; tyrosine-specific protein kinase
F:423-686/Domain: protein kinase homology <KIN>
F:431-439/Region: protein kinase Arp-binding motif

Query Match 8.5%; Score 82; DB 2; Length 1009;
Best Local Similarity 26.9%; Pred. No. 18;

```

Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
Oy 88 EFKNIGSGLLMANIDLEKSR-----TGDEILPRGLELYVEECTCEDCIKSKPKV 138
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 249 KFFNT---LAFGANIDQETVRCLELGQGNWITVDIVLIGKGRITSLTSDTKPTCKAEFKQI 305
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 139 DSDHCFPLPAME-----EGATILVTKTKND-----YCK 166
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 RSRICLPLEETQAVLQIGIEGAPOSLSIKTSSLAENMADLIDGYCR 353
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
28669
surface protein 51C - Parametium tetraurelia
C:Species: Parametium tetraurelia
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C:Accession: J28669
R:Nielsen, E.; You, Y.; Forney, J.
J. Mol. Biol. 222, 835-841, 1991
A:Title: Cysteine residue periodicity is a conserved structural feature of variable surf
A:Accession: J28669
A:Reference number: 220504; MUID:92106337; PMID:11762150
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2233 <NE>
A:Cross-references: EMBL:M55164; NID:g159974; PID:g159975; PIDN:AAA61740.1
C:Genetics:
A:Genetic code: SGCS

Query Match 8.5%; Score 81.5; DB 2; Length 2233;
Best Local Similarity 25.1%; Pred. No. 45;
Matches 43; Conservative 17; Mismatches 58; Indels 53; Gaps 10;
Oy 6 GGCSCNEFFDLSLHACIFCQLRCSSNTPPLTCQRCNA-SYTNYSKGNAILMLTCLGLSL 64
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 520 GSCYOKQ-----CSAASQDNTHAACOEYLPACTLSNKKG-----CIDPL 561
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 65 IISLAVFLMFLRKISSEPLKDEFKNTGSGLLGMANIDL-----EKSRTGDEILPRGLE 120
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 562 TCSA-----LIYENELKANREK---CGHTGTCVDIVCTTAFTKTD-----D 603
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 121 YVEECTC---EDCIKSKPKVSDHCFPLPAMEGATI-----LVTTKTN 162
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 604 YVEICEAYKPSNSCV---PNCCKKGCMELAKCESRTIKKQCDVAGKRTN 651
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
D89010
protein R08F11.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C:Accession: D89010
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biologic
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: See websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D89010
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-773 <STO>
A:Cross-references: GB:chr V; PIDN:AAB54249.1; PID:g2088832; GSPDB:GN00023; CESP:R08F11
A:Note: Similar to peroxidase
C:Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 8.4%; Score 81; DB 2; Length 773;
Best Local Similarity 21.7%; Pred. No. 17;
Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6;

```

```

OY 23 PCOLRCSNNPELPLCO-----RYCN-----ASTVNSVKRTNMLLWTCCL---GLSL 64
Db 184 PPKSNATCQGGPKKSCSDPDVHDIRISTGYCCNNRCKPQVANSIRRLRLGLTSTYDGLQA 243
OY 65 IISLAVFVIMFLKRIKISEPLKDEFKNTG--SGLLGMANIDLEKSRGTDEILIPRGLEYTV 123
Db 244 IIRNSVYGSPLPSTRLLISNKLHDEGSTPNPSPVNNLHMQIGQI IADIDILFMPBSTAKDG 303
OY 124 EECTCEDCIKSKPKVDSOHCPEPLPAMEGATILVTTKTDNCKSLPALSA-----TE 176
Db 304 SLLNCTSC--SSPTTISTNCAPIPADADKRYFTEVSRTEACIRLTRALNGOSGQVARTO 361
OY 177 IEKS 180
Db 362 IDON 365

RESULT 8
S60248
protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - human
N:Alternate names: cell adhesion kinase-beta
C:Species: Homo sapiens (man)
C:Date: 10-Apr-1996 #sequence revision 27-Feb-1997 #text_change 17-Nov-2000
C:Accession: S60248; G02330; B57434
R:Lev, S.; Moreno, H.; Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.; Ploewman
Native 376, 737-745, 1995
A:Title: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion ch
A:Reference number: S60248; MUID:95379967; PMID:7544443
A:Accession: S60248
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1009 <LEV>
A:Cross-references: EMBL:U33284; NID:9988304; PIDN:AAC50203.1; PID:9988305
R:Sasaki, T.; Nagura, K.; Sasaki, H.
submitted to the EMBL data library, December 1995
A:Reference number: H01067
A:Accession: G02330
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-22, 'G', 24-434, 'L', 436-1009 <SAS>
A:Cross-references: EMBL:U34522; NID:g1165218; PIDN:AAC05330.1; PID:g1165219
R:Sasaki, H.; Nagura, K.; Ishino, M.; Tobitoka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A:Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-r
A:Reference number: A57434; MUID:95403356; PMID:7673154
A:Accession: B57434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-22, 'G', 24-150 <SA2>
A:Cross-references: GB:D45853; NID:g1000676; PIDN:BA08289.1; PID:d100884; PID:g1000
C:Genetics:
A:Gene: CAKbeta
A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:423-666/Domain: protein kinase homology <KIN>
F:431-439/Region: protein kinase ATP-binding motif

Query Match 8.2% Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 31;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

OY 88 EERNKSGGLGMANIDLEKSR-----TGEDEILPRGLEYVEECTCEDCIKSKPKV 138
Db 249 KFFNT---LAGFANINDQETRYRECELIQGNMITYDLVIGRKGIRQLSLSDQAKPTCLAEFKQI 305
OY 139 DSDHCPPLPAMEGATIL 156
Db 306 RSIRCLPL---EEGOAVL 320

RESULT 9
T43251
furin (EC 3.4.21.75) - fall armyworm

```

N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
 C:Species: Spodoptera frugiperda (fall armyworm)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C:Accession: T43251
 R:Cieplik, M.; Klenk, H.
 submitted to the EMBL Data Library, January 1996
 A:Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
 A:Reference number: 223368
 J:Accession: T43251
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Accession: T43251
 A:Molecule type: mRNA
 A:Residues: 1-1299 <CIE>
 A:Cross-references: EMBL:Z68888; NID:q16785; PID:e219690; PIDN:CAA93116.1
 A:Experimental source: clone Sturin 6; ovary
 C:Function:
 A:Description: responsible for the endoproteolytic processing of proproteins with specif
 C:Keywords: hydrolase; serine proteinase

Query Match 8.2% Score 79.5; DB 2; Length 1299;
 Best Local Similarity 24.1% Pred. No. 40;
 Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;
 Oy 8 CSNPFSLHACIPCOLRCS-----SNTPPLTCQRYCNAS---VNSYKGTNALI-W 57
 Db 1150 CSRPLRIDLNQCVPC--CSERCVTSTPTPD-CCHCNBNGECINSSVAGKRRIAEW 1205
 Oy 58 TGLGS-----LIISLAV-----FVLMFLRKISSEPLDEFKNTGSGLLGMAN 101
 Db 1206 GALHTAPASADAPVAVVTIACAAVGLFITLVVLAHSPREKTKRTKTSVRC----- 1259
 Oy 102 IDLEKSRGTDEILPR-CLEVTVECTCEDCIKSKPKVDSOH 142
 Db 1260 --VEYSR-----LPRTDVETV-----LTSCTDQGPVEYEH 1289

RESULT 10
 D64469
 potassium channel homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: D64469
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Retch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Metrick, J.M.; Glodek, A.;
 Iron, J.D.; Sedow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:9637999; PMID:8688087
 A:Accession: D64469
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-343 <BDJ>
 A:Cross-references: GB:U67575; GB:L77117; NID:g1591992; PIDN:AA899365.1; PID:g1592000; T
 C:Genetics:
 A:Map position: REV1308326-1307295
 C:Superfamily: conserved hypothetical protein s110993

Query Match 8.1% Score 78.5; DB 2; Length 343;
 Best Local Similarity 20.4% Pred. No. 13;
 Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;
 Oy 12 EYPSLHACIPCOLRCSNTPPLTCQRYCNASVNSYKGTNALIWTCLSLIISLAVF 71
 Db 32 DYFALYFVSF-----TITTTGYGDFPTPTFTGLRLLTVVYLCVGVIMVLFSL 80
 Oy 72 VLMLF-----LRKISS--EPLKDEFKNTGSGLLGMA-----NIDLEKSRGTD 111
 Db 81 IAEIVGKEEFYRLKMKMKIKTLKNDHYIICGRLGKVGKEFELEENPFAIDINE 140
 Oy 112 EII-----LPRGLETVVECTCEDCIKSKPKV-----SDPHCF-PLPAMEEG 152
 Db 141 DVLAEYKYDKFLYIYGDAKKEVRL-KAKIDKAKGLITLPSDADNVLTITLARELN 199

Oy 153 ATILVTKTND 163
 Db 200 FNILITAKADE 210

RESULT 11
 JCS894
 killer cell inhibitory receptor p91A precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999
 C:Accession: JCS894
 R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; O
 J. Biochem. 123, 358-368, 1998
 A:Title: Genomic structures and chromosomal location of p91, a novel murine regulator
 A:Reference number: JCS894; MUID:98218758; PMID:9538215
 A:Accession: JCS894
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-841 <YAM>
 A:Cross-references: GB:AF040946
 C:Comment: This protein function as inhibitory cell-surface molecule against cell act
 C:Genetics:
 A:Map position: 7
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>
 F:24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #statu
 F:636-674/Domain: transmembrane #status predicted <TM>
 F:675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 8.1% Score 78; DB 2; Length 841;
 Best Local Similarity 22.7% Pred. No. 35;
 Matches 46; Conservative 32; Mismatches 61; Indels 64; Gaps 9;
 Oy 9 SONEFDSLHACIPCOLRCS-----SNTPPLTCQRYCNASVNSYKGTNALIWTCLGSL 64
 Db 598 AONSSFYLLSSASAPVELTVSGPIETSTPPT-----MSMPLGGLMTLKLALIGSV 649
 Oy 65 IISLAVFVLMFL--RKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEILPRG---- 118
 Db 650 AFILFIFILIFILRLRRRGRFRDYGKEK-----DLQSSGAEPIITRKGLGQK 699
 Oy 119 -----LETVVECTCEDCIK-----SKRVDSDFCPPLPAMEGATILVTKTN 162
 Db 700 RPNPAATQESLIVASVDMQTEGVLELNSWTPEED-----PQGET----- 741
 Oy 163 DYCKSLPAAL-SATEIEKSISAR 184
 Db 742 -YAOVKPSRLKAKHVSFVSAR 763

RESULT 12
 D86345
 hypothetical protein F16P4.10 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C:Accession: D86345
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar,
 anson, N.F.; Hughes, B.; Huzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: D86345
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-738 <STO>
 A:Cross-references: GB:AE005172; NID:98920639; PIDN:AAF81361.1; GSPDB:GN00141
 C:Genetics:

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:49:26 ; Search time 15.794 Seconds
(without alignments)
483.199 Million cell updates/sec

Title: US-09-848-271-2
Perfect score: 964
Sequence: 1 MDAQGQCSQNEYFDLHA.....CKSLPALSAIEKISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	TR17_HUMAN	002223 homo sapien
2	572	59.3	185	TR17_MOUSE	088472 mus musculi
3	116.5	12.1	175	T13C_MOUSE	0948d0 mus musculi
4	94	9.8	323	TNR6_BOVIN	P51867 bos taurus
5	93	9.6	184	T13C_HUMAN	096rj3 homo sapien
6	86.5	9.0	867	PROM_MOUSE	054990 mus musculi
7	82	8.5	1009	FAK2_MOUSE	094vp9 m protein t
8	82	8.5	1009	FAK2_RAT	P70600 rattus norv
9	79.5	8.2	1009	FAK2_HUMAN	014289 h protein t
10	78.5	8.1	293	T13X_HUMAN	014836 homo sapien
11	78.5	8.1	343	Y057_METJA	058752 methanococ
12	77	8.0	249	T13X_MOUSE	09etj3 mus musculi
13	75.5	7.8	638	YCSB_SCHPO	074910 schizosacch
14	75	7.8	849	SRK6_BRAOL	009092 brassica ol
15	74.5	7.7	384	ERL1_KLULA	P41771 kluyveromyc
16	72.5	7.5	1013	PRML_DROME	P82295 drosophila
17	71.5	7.4	105	Y078_NPYOP	010331 oryza pesu
18	71.5	7.4	627	Y017_RICPR	092ec6 rickettsia
19	71	7.4	227	COMB_THEMEA	09w2q4 thermotoga
20	70.5	7.3	188	Y101_UREPA	09p443 ureaplasma
21	70.5	7.3	1203	MGR5_RAT	P31424 rattus norv
22	70.5	7.3	1877	PKC5_MOUSE	004592 mus musculi
23	70.5	7.3	2715	G156_PAPPR	P13837 paramesit
24	70	7.3	654	H570_TRIRU	093866 trichophyto
25	69.5	7.2	573	T1PC_BACSU	P39209 bacillus su
26	69.5	7.2	1212	MGR5_HUMAN	P41594 homo sapien
27	69.5	7.2	5376	ZAN_MOUSE	088799 mus musculi
28	69	7.2	324	GCL_MOUSE	P01868 mus musculi
29	69	7.2	352	C5AR_RAT	P97520 rattus norv
30	69	7.2	379	PANE_YEAST	P38787 saccharomyc
31	69	7.2	393	GCLM_MOUSE	P01869 mus musculi
32	69	7.2	416	R23B_MOUSE	P54728 mus musculi
33	68.5	7.1	321	OSV1_HUMAN	Q9ugf6 homo sapien

ALIGNMENTS

RESULT 1	ID	TR17_HUMAN	STANDARD:	PRT:	184 AA.	
AC	002223:					
DT	01-JUL-1993 (Rel. 26, Created)					
DT	01-JUL-1993 (Rel. 26, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).					
DE	TNFRSF17 OR BCM4 OR BCM.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxId=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.					
RC	TISSUE=peripheral blood leukocytes, and lymph node;					
RX	MEDLINE=93010984; PubMed=1396583;					
RA	Laabi Y., Gras M.P., Cardonnel F., Brouet J.C., Berger R.,					
RA	Larsen C.J., Tsapis A.;					
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene					
RT	by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";					
RL	EMBO J. 11:3897-3904(1992).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=94218235; PubMed=8165126;					
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;					
RT	"The BCM gene, preferentially expressed during B lymphoid					
RT	maturation, is bidirectionally transcribed.";					
RL	Nucleic Acids Res. 22:1147-1154(1994).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=99425270; PubMed=10493829;					
RA	Lofthus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,					
RA	Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,					
RA	Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,					
RA	Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;					
RT	"Genome duplications and other features in 12 Mb of DNA sequence from					
RT	human chromosome 16p and 16q.";					
RL	Genomics 60:295-308(1999).					
RN	[4]					
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.					
RX	MEDLINE=21419161; PubMed=11528522;					
RA	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;					
RT	"Presence of four major haplotypes in human BCM gene: lack of					
RT	association with systemic lupus erythematosus and Rheumatoid					
RT	arthritis.";					
RL	Genes Immun. 2:276-279(2001).					
RN	[5]					
RP	FUNCTION.					
RX	MEDLINE=20363816; PubMed=10903733;					
RA	Hatzoglou A., Roussel J., Bourgade M.-F., Rogier E., Madry C.,					
RA	Inoue J., Devergne O., Tsapis A.;					
RT	"TNF receptor family member BCM4 (B cell maturation) associates with					
RT	TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and					
RT	activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38					

34	68.5	7.1	328	1	Y679_CHILMU	Q9p1z7 chlamydia m
35	68.5	7.1	409	1	R23B_HUMAN	P54727 homo sapien
36	68.5	7.1	575	1	CH62_CUCMA	O05046 cucurbita m
37	68.5	7.1	576	1	CH62_MAITE	O43298 zea mays (m
38	68.5	7.1	577	1	CH61_MAITE	P29185 zea mays (m
39	68	7.1	590	1	ACCD_PEA	P18823 pisum sativ
40	68	7.1	1140	1	RA18_SCHPO	P53692 schizosacch
41	68	7.1	1203	1	XOPE_XENLA	P50533 xenopus lae
42	68	7.1	2158	1	MY9B_HUMAN	O13459 homo sapien
43	68	7.1	3386	1	POLG_DENK	P09866 d genome po
44	67.5	7.0	178	1	LACB_BOVIN	P02754 bos taurus
45	67.5	7.0	245	1	YH77_ARCFU	O28497 archaeoglob

RT milogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE-20259066; PubMed-10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 Harrison K., Kinsvogel W., Clegg C.H.;
 RA "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RT Nature 404:995-999(2000).
 RL [7]
 RN FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RP MEDLINE-21170294; PubMed-10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollin M.,
 Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;
 RA "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
 RT humoral immunity.";
 RT Nat. Immunol. 1:252-256(2000).
 RL [8]
 RN INTERACTION WITH TRAF5 AND TRAF6.
 RP MEDLINE-20381353; PubMed-10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 CC EMBL; 214954; CAAT7679.1; -
 DR EMBL; 229575; CAAB2691.1; -
 DR EMBL; 229574; CAAB2690.1; -
 DR EMBL; 095742; AAB67251.1; -
 DR EMBL; AB052772; BAB60895.1; -
 DR PIR; S31208; S31208.
 DR PIR; S31209; S31209.
 DR Gene; HGNC:11913; TNFRSF17.
 DR MIM: 109545; -
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 KW DOMAIN 1 54
 FT TRANSMEM 55 77
 FT DOMAIN 1 54
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT BREAKPOINT FOR TRANSLOCATION TO FORM
 FT INTERLEUKIN 2/BCM ONCOGENE.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT A -> T.
 FT /FTID=VAR_012234.
 FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1,3e-83;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MLOMACGCSQNEFYDLSLHACIPQCRSSNPPPLTCORCNASVSNVSGKTNAILMTCL 60
 DB 1 MLOMACGCSQNEFYDLSLHACIPQCRSSNPPPLTCORCNASVSNVSGKTNAILMTCL 60
 OY 61 GSLIISLAVFYLMFLRRKISSRPLKDEFRKNGSGILGMANDLERSRGTDEILPRGLE 120
 DB 61 GSLIISLAVFYLMFLRRKISSRPLKDEFRKNGSGILGMANDLERSRGTDEILPRGLE 120
 OY 121 YVEEECTCEDCIKSKRPVSDHCFPLPAMEGATILVTTRKNDYCKSLPAALSAITEERS 180
 DB 121 YVEEECTCEDCIKSKRPVSDHCFPLPAMEGATILVTTRKNDYCKSLPAALSAITEERS 180
 OY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 2
 TR17_MOUSE STANDARD; PRT; 185 AA.
 ID TR17_MOUSE
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 GN maturation protein).
 OS TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN-BALB/C; TISSUE-Spleen;
 RP MEDLINE-99061155; PubMed-9846698;
 RX Mady C., Laab Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Coniat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN-C57BL/6J; TISSUE-Colon;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamaki I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
 RA Kueth P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Batsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlay M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by

CC similarity).

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are

CC produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and

CC heart, and at lower levels in kidney and lung.

CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

CC -----

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CC -----

DR EMBL: AF061505; AAC23799.1; -

DR EMBL: AK020247; BAB32038.1; -

DR MGI: 1343050; Tnftrsf17.

KM Receptor: Immune response; Signal-anchor; Transmembrane;

KM Alternative splicing

FT DOMAIN 1 49

FT TRANSMEM 50 70

FT DOMAIN 71 185

FT REPEAT 4 36

FT DISULFID 5 18

FT DISULFID 21 32

FT DISULFID 25 36

FT VARSPLIC 87 91

SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 59.3%; Score 572; DB 1; Length 185;

Best Local Similarity 62.6%; Pred. No. 8.7e-47;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MACQCSQNEYFDLHACIPQCRSCSNTPPLTCQRYCNASVYNGTNAIIMTCGLS 63

DB 1 MACQCHSEYFDLHACIKRCHLRCSN--PPATCQPCYCDPSVYNGTIVLIMFGLT 58

QY 64 LIISLAVFLMFLTKRISSEPLKDEFKN---TGSGLGNANIDLEKSRNGDEIILPRL 119

DB 59 LVLSLALFTISFLRKKNPEALKDEPQSPQLDGSALQDKADELFRIRAGDDRIEPRSL 118

QY 120 EYVVECTCQDCIKSKRYVSDHCFLPAMEEGATILVTTRKTDYCK-SLPAL-SATEI 177

DB 119 EYVVECTCEDCVKSKRPGSDHFFLPAMEEGATILVTTRKTDYCKSVPTALQSYGM 178

QY 178 EKSIAR 184

DB 179 EKPTHR 185

RESULT 3

T13C.MOUSE STANDARD: PRT: 175 AA.

AC 09DBD0;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Tumor necrosis factor receptor superfamily member 13C (B cell-

DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor

DE 3) (B-cell maturation defect).

GN TNFRSF13C OR BAFFR OR BCMD OR BR3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN=BALE/C; TISSUE=B-cell lymphoma;

RX MEDLINE=21442025; PubMed=11509692;

KM Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,

RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,

RA Strauch K., Zafarali M., Benjamin C.D., Tschopp J., Browning J.L.,

RA Ambrose C., a newly identified TNF receptor that specifically interacts

RT "BAFF-R" with BAFF.";

RL Science 293:2108-2111(2001).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.

RC STRAIN=A/J;

RX MEDLINE=21475520; PubMed=11591325;

RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,

RA Cancro M.P., Grewal I.S., Dixit V.M.;

RT Identification of a novel receptor for B lymphocyte stimulator that

RT is mutated in a mouse strain with severe B cell deficiency.";

RL Curr. Biol. 11:1547-1552(2001).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirni L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Futuro M., Aono H., Balderelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carolini P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [4]

RP FUNCTION.

RX MEDLINE=21614654; PubMed=11747827;

RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,

RA Hilbert D.M., Hayes C.E., Cancro M.P.;

RT *Competition for Blys-mediated signalling through Bcmd/BR3 regulates

RT peripheral B lymphocyte numbers.";

RL Curr. Biol. 11:1986-1989(2001).

CC -1- FUNCTION: B-cell receptor specific for TNFSF13B/TAL1/BAFF/Blys.

CC Promotes the survival of mature B-cells and the B-cell response.

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are

CC produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;

CC detected at lower levels in lung and thymus.

CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell

CC deficiency. B-cell deficient strain A/MySJ has a 4.7 kb insertion

CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA

CC is not detectable. B-cell lymphopoiesis is normal, but the life

CC span of peripheral B-cells is much reduced.

CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

CC -----

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CC -----

DR EMBL: AF373847; AAK91827.1; -

DR EMBL: AK008142; BAB25490.1; -

DR MGI: 1919299; Tnftrsf13c.

KM Receptor: Immune response; Signal-anchor; Transmembrane; Glycoprotein;

KW Alternative splicing.
 FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 92 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 38 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 133 143 MISSING (IN ISOFORM 2).
 SO SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FE87FE CRC64;
 Query Match 12.18; Score 116.5; DB 1; Length 175;
 Best Local Similarity 29.48; Pred. NO. 0.00051;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
 OY 7 QCSGNEVFDLSLHACIPCOL-----RCSSNTPPLTQGRCNMSYNSVYK---GTNAIL 56
 DB 21 QCNQTECFDPLVNCVSELFTPTDGTHTSSLEPGTALQPEGNALRPDVALLVGAPALL 80
 OY 57 WTCLGLSLI--ISLAVFLMFLRKIS--SEPLKDEKNTGSGLLGMANIDLEKSRIGD 111
 DB 81 GLIALTLVGLVSLVSMWRQGLRTASPDTSSEGVQGE-----SLENVFVPSSE-- 129
 OY 112 EIIIPRGLEYVEECTGECDCIKSKPKVDSDHCFPLPAMEGATILVTTKT 161
 DB 130 ---PHASAPTPPLK-EDADSALPR---HSVPVPAETELGSTELVTTKT 170
 RESULT 4
 TNFR6_BOVIN STANDARD; PRT; 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66226401; PubMed=8634151;
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.,"
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC -----

DR EMBL: U34794; AAC48546.1; -.
 DR HSSP; P25445; IDDF.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR Pfam: PF00531; death; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR Receptor: Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 323
 FT DOMAIN 17 170
 FT TRANSMEM 171 188
 FT DOMAIN 189 323
 FT REPEAT 45 80
 FT REPEAT 81 124
 FT REPEAT 125 163
 FT DOMAIN 238 306
 FT DISULFID 45 56
 FT DISULFID 57 70
 FT DISULFID 60 79
 FT DISULFID 82 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 140
 FT DISULFID 143 154
 FT DISULFID 146 162
 FT CARBOHYD 38 38
 FT CARBOHYD 115 115
 SO SEQUENCE 323 AA; 36445 MW; 4D8BA90E9E1F4892 CRC64;
 Query Match 9.88; Score 94; DB 1; Length 323;
 Best Local Similarity 22.18; Pred. NO. 0.13;
 Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;
 OY 8 CSQ-NEVFDLSLHA--CIPCOL-----RCSSN-----T 32
 DB 82 CSEGNEYTDKSHSDKRCRCICDEHGLEVEQNCRTTRNTKCKSMFPCSSPCEHCN 141
 OY 33 PLPTCO---RYCNASVNSVKGNTNA--ILMTCGLSLIISLAVFLMFLRKISSEPL 85
 DB 142 PCTTCEHIIIEKPTPTSTKCKGSRSHANSJMAL---LILLIPVILIVVAVSRERNK 197
 OY 86 KDEKNTGSG-----LGMANIDL-----EKSRIGD--EIIIPRGLEYVEECTGCD 130
 DB 198 KNDYCNASASNDGROJLNTVDVILGKYTPSIADQMRTVEKFKKNGM---EAKIDD 253
 OY 131 CIKSKPKVDSHCFPLPAMEGATILVY-----TKTNDYC---KSLPAALS 173
 DB 254 IMH-----DNVH-----ETAEOKVQLRNWQSHGKKNAVCTLTSLPAPALA 295
 RESULT 5
 TNFR3C_HUMAN STANDARD; PRT; 184 AA.
 AC Q96R33;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3).
 DE TNFRSF13C OR BAFFR OR BR3.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 CC -----

RC TISSUE-B-cell lymphoma;
 RX MEDLINE-21442025; PubMed-11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Millen C.,
 RA Struchiner K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RT *BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF*;
 RL Science 293:2108-2111(2001).
 RN [2]
 RP FUNCTION.
 RX MEDLINE-21475520; PubMed-11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
 RA Cancro M.P., Grewal I.S., Dixit V.M.;
 RT Identification of a novel receptor for B lymphocyte stimulator that
 RT is mutated in a mouse strain with severe B cell deficiency*;
 RL Curr. Biol. 11:1547-1552(2001).
 CC -1- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
 CC in resting B-cells. Detected at lower levels in activated B-cells,
 CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL: AE373846; AAK91826.1; -;
 DR Gene: HGNC:17755; TNFRSF13C.
 DR MIM: 606269; -;
 DR PROSITE: PS00652; TNFR_NGFR_1; FALSE_NEG.
 DR PROSITE: PS50050; TNFR_NGFR_2; FALSE_NEG.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing.
 FT DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 79 99 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 18 35 TNFR-CYS (PARTIAL).
 FT DISULFID 19 32 BY SIMILARITY.
 FT DISULFID 24 35 BY SIMILARITY.
 FT VARSPLIC 143 143 P -> PA (IN ISOCOREM 2).
 SQ SEQUENCE 184 AA; 18863 MW; F2BFB9809A27138 CRC64;
 Query Match 9.6%; Score 93; DB 1; Length 184;
 Best Local Similarity 26.5%; Pred. No. 0.088;
 Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

RESULT 6
 PROM MOUSE
 ID PROM MOUSE STANDARD; PRT; 867 AA.
 AC 054990; 035408;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prominin precursor (Antigen AC133 homolog).
 GN PROM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Miraglia S., Godfrey W., Buck D.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE-98024147; PubMed-9356465;
 RA Weigmann A., Corbell D., Hellwig A., Huttner W.B.;
 RT Prominin, a novel microvilli-specific polytopic membrane protein of
 RT the apical surface of epithelial cells, is targeted to plasmalemma
 RT protrusions of non-epithelial cells*;
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED ON THE APICAL SIDE OF
 CC NEUROEPITHELIAL CELLS AND OF OTHER EPITHELIA SUCH AS LUNG BUDS,
 CC GUT AND URETER BUDS. IN THE ADULT, EXPRESSED AT THE APICAL SIDE
 CC OF THE KIDNEY TUBULES AND OF THE EPENDYMAL LAYER OF THE BRAIN. NOT
 CC EXPRESSED IN GUT, LIVER, LUNG, PITUITARY, ADRENAL, HEART OR
 CC SPLEEN.
 CC -1- SIMILARITY: BELONGS TO THE PROMININ FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF039663; AAB96916.1; -;
 DR EMBL: AF026269; AAB86715.1; -;
 DR MGD: MGI:1100886; Prom.
 KW Signal; Transmembrane; Glycoprotein.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 867 PROMININ.
 FT DOMAIN 20 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 128 POTENTIAL.
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 179 POTENTIAL.
 FT DOMAIN 180 434 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 435 455 POTENTIAL.
 FT DOMAIN 456 487 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 488 508 POTENTIAL.
 FT DOMAIN 509 794 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 795 815 POTENTIAL.
 FT DOMAIN 816 867 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 868 885 POTENTIAL.
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 732 732 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 732 732 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 64 64 S -> N (IN REF. 2).
 FT CONFLICT 84 84 K -> N (IN REF. 2).
 FT CONFLICT 94 102 MISSING (IN REF. 2).
 FT CONFLICT 668 668 P -> L (IN REF. 2).
 FT CONFLICT 668 668

FT CONFLICT 844 844 G -> D (IN REF. 2).
 SQ SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;
 Query Match 9.0%; Score 86.5; DB 1; Length 867;
 Best Local Similarity 22.7%; Pred. No. 1.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

OY 18 LHACIPCOLRCSSNTPPLTCORCYCNASTNSVKGNTAIIWTCGLISLIISLAVFVLMFL 77
 DB 126 LVGCFECMCRC-----CNK-CGGEHGOROKNAPCRKCLGLIIVICLLISLIGITY 176
 OY 78 RKISSEPLKDFKNGSGLLGMANIDLEKSRGD-EIIL---PRGLETVEECGE----- 129
 DB 177 GFVANQOTRTIKGTQK-----LAKSNRDFOTLTPTPOIDVVEQYVTKRKA 227
 OY 130 ----DCIKS-----KPRVSDHCFPLPAMEGATIIIVTK-TNDYCKSLPAL-- 172
 DB 228 FSDLDGISVLCGRICKDLPKRV-----TPVLEIRAMATIKQTDALQNMSSSLKS 280
 OY 173 ---SATEIEKISIA 183
 DB 281 LDATATQIINTNLS 294

RESULT 7
 FAK2_MOUSE STANDARD: PRT; 1009 AA.
 ID FAK2_MOUSE
 AC Q9QV99;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase beta) (CAK beta) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase 2) (Calcium-dependent tyrosine kinase) (CADTK) (Related adhesion focal tyrosine kinase).
 DE PIK2B OR FAK2 OR PYK2 OR RAFTK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=6070905; Pubmed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S., Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RT "Identification and characterization of a novel related adhesion focal tyrosine kinase (RAFTK) from megakaryocytes and brain.";
 RT J. Biol. Chem. 270:27742-27751(1995).
 RL [2]
 RN PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCISTIN.
 RX MEDLINE=21396557; Pubmed=11493697;
 RA Benzling T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers phosphorylation of Pyk2.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 RL
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the downstream signals that regulate neuronal activity. Interacts with the SH2 domain of Grb2. May phosphorylate the voltage-gated potassium channel protein Kv1.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase activity (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas), Nephrocystin and GTPase regulator associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin induces the membrane-association of the kinase.
 CC -1- PTM: Phosphorylated on tyrosine in response to various stimuli that elevate the intracellular calcium concentration, as well as

CC by PKC activation. Recruitment by Nephrocystin to cell matrix
 CC adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 CC SUBFAMILY.
 CC HSSP: P08631; IAD5.
 DR MGD: MGI:104908; Pk2b.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR005189; Focal_AT.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF03623; Focal_AT; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Euk_Pkinase; 1.
 DR SMART: SM00295; B41; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation.
 FT DOMAIN 425 683
 FT NP_BIND 431 439 ATP (BY SIMILARITY).
 FT BINDING 457 457 ATP (BY SIMILARITY).
 FT ACT_SITE 549 549 BY SIMILARITY.
 FT DOMAIN 701 767
 FT DOMAIN 831 869 PRO-RICH.
 FT DOMAIN 868 1009 FOCAL ADHESION TARGETING (FAT).
 FT MOD_RES 402 402 PHOSPHORYLATION.
 FT MOD_RES 579 579 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 1009 AA; 115821 MW; 963959FF56DF9605 CRC64;

Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

OY 88 EFKWTGSGLLGMANIDLEKSR-----TGDEIIIPRGLEYVEECTCEKIKSRPV 138
 DB 249 KFFNT---LAFANIDQTYRCGLGQWNTIVDLVIGPKGRQLTSQDTKPTCLAEPFOI 305

OY 139 DSDHCFPLPAME-----EGATIIIVTKTND-----YCK 166
 DB 306 RSIRCLPLETQAVLQIGEGAPQSLSTKTSLSAEENMADLDGYCR 353

RESULT 8
 FAK2_RAT STANDARD: PRT; 1009 AA.
 ID FAK2_RAT
 AC P70600; Q63201; O88489;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase 2) (CAK beta) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase 2) (Calcium-dependent tyrosine kinase) (CADTK).
 DE PIK2B OR FAK2 OR PYK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE-Liver epithelium;
 RX MEDLINE=97094711; Pubmed=8939945;
 RA Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L., Wilim M., Anderregg R.J., Graves L.M., Barp H.S.;
 RT "Activation of a novel calcium-dependent protein-tyrosine kinase. Correlation with c-Jun N-terminal kinase but not mitogen-activated protein kinase activation.";
 RT J. Biol. Chem. 271:29993-29998(1996).

RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE-95403356; PubMed-7673154;
 RA Sasaki H., Nagura K., Ishino M., Tobiooka H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
 RP DOMAIN.
 RC TISSUE-Hippocampus;
 RX MEDLINE-98311659; PubMed-9645946;
 RA Xiong W.-C., Macklem M., Parsons J.T.;
 RT "Expression and characterization of splice variants of PYK2, a focal
 RT adhesion kinase-related protein.";
 RL J. Cell Sci. 111:1981-1991(1998).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neurotrophide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Isoform 1, but not isoform 2, interacts with Crk-
 CC associated substrate (Cas), Nephrocystin and GTPase regulator
 CC associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase (By similarity).
 CC Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/PYK2 and
 CC 3/PYK2s; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
 CC brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
 CC in the spleen and other tissues, whereas isoforms 2 and 3 are
 CC expressed in the spleen and brain (highest in cerebellum).
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 CC that elevate the intracellular calcium concentration, as well as
 CC by PKC activation. Recruitment to Nephrocystin to cell matrix
 CC adhesions initiates Tyr-402 phosphorylation (By similarity). In
 CC monocytes, adherence to substrata is required for tyrosine
 CC phosphorylation and kinase activation. Angiotensin II,
 CC thapsigargin and L-alpha-Lysophosphatidic acid (LPA) also induce
 CC autophosphorylation and increase kinase activity.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 CC SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U69109; AAC52895.1; -
 CC EMBL: D45854; BAA08290.1; -
 CC EMBL: AF063890; AAC28340.1; -
 CC HSSP: P00523; 2PTR.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC InterPro: IPR001589; Focal_AT.
 CC Pfam: PF00069; pkinase.1.
 CC Pfam: PF03623; Focal_AT.1.
 CC ProDom: PD0000001; Euk_pkinase.1.
 CC SMART: SM00295; BAI; 1.
 CC SMART: SM00219; TYRK; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
 KM Alternative splicing.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 457 457
 FT ACT_SITE 549 549
 FT DOMAIN 701 767
 FT DOMAIN 831 869
 FT DOMAIN 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 579 579
 FT VARSPPLIC 1 771
 FT VARSPPLIC 772 780
 FT VARSPPLIC 739 780
 FT CONFLICT 205 205
 FT CONFLICT 807 807
 SQ SEQUENCE 1009 AA; 115784 MW; D435A4758CA49E9B CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
 OY 88 EFKNTGSGILGMANIDLEKSR-----TGDEIILPRGLTYVECTCEDCIKSKPV 138
 DB 249 KFFNT---LAGFANIDETRYRCGLGCMNTVDLVICPKRIQDTSQDTKPTLAERKQI 305
 OY 139 DSDHCPELPAME-----EGATLVTKTND-----YCK 166
 DB 306 RSIRCLPLEFETQAVLQLGIEGAPQSISIKTSLSAEENMADLDGYCR 353
 RESULT 9
 ID FAK2_HUMAN STANDARD; PRT; 1009 AA.
 AC .Q14289; Q16709; Q13475; Q14290;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (focal adhesion kinase
 DE 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 DE beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
 DE adhesion focal tyrosine kinase).
 GN PKK2B OR FAK2 OR PYK2 OR RAFTK.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Brain;
 RX MEDLINE-95379967; PubMed-7544443;
 RA Lev S., Moreno H., Martinez R., Canoil P., Peles E., Musacchio J.M.,
 RA Ploman G.D., Rudy B., Schlessinger J.;
 RT "Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation
 RT of ion channel and MAP kinase functions.";
 RL Nature 376:737-745(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Hippocampus;
 RX MEDLINE-96435932; PubMed-8838818;
 RA Herzog H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
 RT "Molecular cloning and assignment of FAK2, a novel human focal
 RT adhesion kinase, to Bp11.2-p22 by nonisotopic in situ hybridization.";
 RL Genomics 32:484-486(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Hippocampus;
 RX MEDLINE-95403356; PubMed-7673154;
 RA Sasaki H., Nagura K., Ishino M., Tobiooka H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).

RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hilegowdara D., Li J., Jiang S.,
 RA Paszor L.M., White R.A., Groopman J.E., Avraham H.;
 RT "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain";
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Monocytes;
 RX MEDLINE=98211954; PubMed=9545257;
 RA Li X., Hunter D., Morris J., Haekill J.S., Earp H.S.;
 RT "A calcium-dependent tyrosine kinase splice variant in human
 RT monocytes. Activation by a two-stage process involving adherence and a
 RT subsequent intracellular signal";
 RL J. Biol. Chem. 273:9361-9364(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N.,
 RA Menzel U., Schlihael M.B., Wen G., Taudien S., Rosenthal A.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PHOSPHORYLATION OF TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
 RP WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; PubMed=11493697;
 RA Benzling T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocytin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas).
 CC Nephrocytin and GTPase regulator associated with Pak (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocytin
 CC induces the membrane-association of the kinase.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Most abundant in the brain, with highest
 CC levels in amygdala and hippocampus. Low levels in kidney. Also
 CC expressed in spleen and lymphocytes.
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 CC that elevate the intracellular calcium concentration, as well as
 CC by PKC activation. Recruitment by Nephrocytin to cell matrix
 CC adherence initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. PAK
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: U33284; AAC50203.1; -
 CC EMBL: L49207; AAB47217.1; -
 CC EMBL: D45853; BAA08289.1; -
 CC EMBL: U43522; AAC05330.1; -

DR EMBL: S80542; AAB35701.1; -
 DR EMBL: AF311103; -; NOT_ANNOTATED_CDS.
 DR HSSP: P08631; IAD5.
 DR Genew: HGNC:9612; PTK2B.
 DR MIM: 601212; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR005189; Focal_Ar.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF006069; pkinase.1.
 DR Pfam: PF03623; Focal_Ar.1.
 DR Prodom: PD000001; Euk_pkinase.1.
 DR SMART: SM00295; B41.1.
 DR SMART: SM00219; TYKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR Tyrosine-protein kinase: Transferase; ATP-binding; Phosphorylation;
 KW Alternative splicing.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 457 457
 FT ACT_SITE 549 549
 FT DOMAIN 702 767
 FT DOMAIN 831 869
 FT DOMAIN 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 579 579
 FT VARSP_LIC 739 780
 FT MUTAGEN 859 859
 FT CONFLICT 23 23
 FT CONFLICT 256 256
 FT CONFLICT 435 435
 FT CONFLICT 780 780
 SQ SEQUENCE 1009 AA; 115874 MW; 420B21046274E7C2 CRC64;
 Query Match 8.28; Score 79.5; DB 1; Length 1009;
 Best Local Similarity 32.1%; Pred. No. 10;
 Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;
 QY 88 EFKNTGSLGGMANIDLEKSR-----TGDEIIIPRGLEYVECTCEDCKSKPKV 138
 DB 249 KFEFT---LAGEFANIDDTYRCELIDGMNITVDVIGPKGIROLTSODAKPTCIAERKOT 305
 QY 139 DSDHCFFPLPAMEGATIL 156
 DB 306 RSIRCLPL---EEGQAVL 320
 RESULT 10
 T13X_HUMAN
 ID T13X_HUMAN STANDARD; PRT; 293 AA.
 AC 014836;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TACT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; PubMed=9311921;
 RA von Buehlow G.-U., Bram R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.

CC	TISSUE-Blood:
RA	Strausberg R.;
RL	Submitted (Apr-2002) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	FUNCTION.
RX	MEDLINE=20519647; PubMed=10956646;
RA	Mu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA	Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinke D., Lartout D.,
RA	Miyone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA	Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;
RT	"Tumor necrosis factor (TNF) receptor superfamily member TNFR1 is a
RT	high affinity receptor for TNF family members APRIL and BLys.";
RL	J. Biol. Chem. 275:35478-35485(2000).
RN	[4]
RP	FUNCTION.
RA	MEDLINE=21170294; PubMed=10973284;
RA	Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA	McCabe S.E., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA	Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thellin L.F.;
RT	"APRIL and TRAIL-I and receptors BCMA and TNFR1: system for regulating
RT	humoral immunity.";
RL	Nat. Immunol. 1:252-256(2000).
CC	-1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TRAIL/BAFF/BLys
CC	that binds both ligands with similar high affinity. Mediates
CC	calcineurin-dependent activation of NF-kappa-B, as well as activation
CC	of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC	cell function and the regulation of humoral immunity."
CC	-1- SUBUNIT: Blends TRAF2, TRAF5 and TRAF6. Blends the NH2-terminal
CC	domain of CARD with its C-terminus.
CC	-1- SUBCELLULAR LOCATION: Type III membrane protein.
CC	-1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC	intestine and peripheral blood leukocytes. Expressed in resting B-
CC	cells and activated T-cells, but not in resting T-cells.
CC	-1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC	-1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: AF023614; AAC51790.1; -
DR	EMBL: BC028072; AAH28072.1; -
DR	GeneW: HGNC:18153; TNFSF13B.
DR	MIM: 604907; -
DR	InterPro: IPR001368; TNFR_C6.
DR	PROSITE: PS00652; TNFR_NGFR_1; 1.
DR	PROSITE: PSS0050; TNFR_NGFR_2; FALSE_NEG.
KW	Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW	Repeat.
FT	DOMAIN 1 165
FT	DNAIDM 166 186
FT	TRANSMEM 186
FT	EXTRACELLULAR (POTENTIAL).
FT	SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT	(POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	TNFR-CYS 1.
FT	TNFR-CYS 2.
FT	REPEAT 33 67
FT	REPEAT 70 104
FT	TNFR-CYS 1.
FT	DISULFID 34 47
FT	BY SIMILARITY.
FT	DISULFID 50 62
FT	BY SIMILARITY.
FT	DISULFID 54 66
FT	BY SIMILARITY.
FT	DISULFID 71 86
FT	BY SIMILARITY.
FT	DISULFID 89 100
FT	BY SIMILARITY.
FT	DISULFID 93 104
FT	BY SIMILARITY.
FT	CARDORD 128 128
FT	P -> L (IN REF. 2).
FT	CONFLICT 251 251
SO	SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
Query Match	8.1%; Score 78.5; DB 1; Length 293;
Best Local Similarity	19.9%; Pred. No. 3.4;
Matches 41: Conservative	35; Mismatches 73; Indels 57; Gaps 10

```

Oy      8 CSQNDYEPSSLHACIPQOLRCSSNTPPLTCQRYCASTNSVKGK-NAIIMTGLGLSLI 65
        | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      34 CPEDYWPDPILGTCQCKSTKICNHOS-QRTCAFCPSLSICRRERQCKFYDHLRIDTISCASI 92
Oy      66 I-----SLAVEVIMPL-----LKRISSEPLKDEFKNTGSGLLGMANIDLEKS----- 107
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      93 CGQHKQCAAYCCENKLRSPVNLPELRLRQRBGSVEYNNDSNSGR-YQGLEHSGSEASPLP 151
Oy      108 ---RTGDEIILPRG-----LEYVEBCTCEBCKIKSRP-----KYD 139
        | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      152 GLKLSADQVALVYSLGLCLCAVLCCFLVAVACFLKRRGDCPCSCP-RSRPROSPAKSS 209
Oy      140 SDHCFLPAMEGATILVTTKTDNYC 165
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      210 QDH-----AMEAGSPVSTSPERPEYC 230

RESULT 11
YD57_METJA
ID YD57_METJA STANDARD: PROT: 343 AA.
AC Q58752:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative potassium channel protein MJ1357.
GN MJ1357.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota: Methanococci: Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA But C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weissbrock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Georgiades N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG. TO M_JANNASCHII MJ0138.1.
CC -!- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
CC -----
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ID	YCSB_SCHPO	STANDARD:	PRT:	638 AA.
AC	074910;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hypothetical WD-repeat protein C613.12c in chromosome III.			
CS	SPCC613.12C.			
OC	Schizosaccharomyces pombe (fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetes; Schizosaccharomycetaceae;			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RC	MEDLINE:21848401; PubMed=11859360;			
RA	Wood V., Gilliam R., Rafandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Squires J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,			
RA	Geitjes S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holroyd S., Horsbly T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Volckaert G., Aert R., Robben J., Glymoprez B.,			
RA	Wellings I., Vanstreels E., Rieger M., Schefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Wedler H., Wambitt R., Purnelle B.,			
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,			
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Lucas M., Roehet M., Galliardin C., Tallada V.A., Garzon A., Rhode G.,			
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Domiguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,			
RA	Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,			
RA	Shpakowski G.V., Ussery D., Barrett B.G., Nurse P.;			
RL	"The genome sequence of Schizosaccharomyces pombe.";			
RL	Nature 415:871-880(2002).			
CC	-1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).			
CC	-----			
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CC	-----			
DR	EMBL: AL031644; CAA21064.1; -			
DR	InterPro: IPR001680; WD40.			
DR	Pfam: PF00400; WD40; 4			
DR	PRINTS: PR00320; GPROTINRPT.			
DR	SMART: SM00320; WD40; 4.			
DR	PROSITE: PS00678; WD_REPEATS_1; 2.			
DR	PROSITE: PS50082; WD_REPEATS_2; 2.			
DR	PROSITE: PS50294; WD_REPEATS_REGION; 1.			
RV	Hypothetical protein: Repeat: WD repeat.			
FT	REPEAT 297 336 WD 1.			
FT	REPEAT 486 525 WD 2.			
FT	REPEAT 544 583 WD 3.			
FT	REPEAT 587 626 WD 4.			
SQ	SEQUENCE 638 AA; 71536 MW; 6CD360D8748AAF98 CRC64;			

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OY 12 EXPDLSLHACIPCOLRGCSNTPPLTCQRYCNAATNSKGNATLMTGLSLIISLAVF 71
Db 42 EYDFEYRAELPCP-----RPSLSISKSHIAKAPSNKKR-----LEQLLLTSGTF 88
OY 72 VLMEFLRKISSEPLKDEFRKNTGSGILGMANIDLEKSPRTGDEILPRGLEAYVEEC----- 126
Db 89 L-----PNSRPYLSEVRKHTHL-----LSNSITGDCKPPLSHYDFTPEECFLIOE 134
OY 127 -----TCEDCIKSKRPVSDSDHCFFPLPAMEGATILVT 158
Db 135 AKLKGFPVNSVQFNDAYSTHISPKLPRGAYEDC-----QKFELDNSLSPVDKHAHILIRT 190
OY 159 TKTN-----DYCKS 167
Db 191 YKKNKKLLPDYLLKS 204

RESULT 14
SRK6_BRAOL STANDARD; PRT; 849 AA.
ID SRK6_BRAOL Q09092;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
DE (S-receptor kinase) (SRK).
GN SRK6.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots II; Brassicales; Brassicaceae; Brassica.
OX NCBI_taxid=3712;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_56S6; TISSUE=stigma;
RX MEDLINE=92020942; Pubmed=1681543;
RA Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;
RT "Molecular cloning of a putative receptor protein kinase gene encoded
RT at the self-incompatibility locus of Brassica oleracea.*";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).
CC -I- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-
CC FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-LOCUS-
CC SPECIFIC GLYCOPROTEINS. INTERACTION WITH A LIGAND IN THE
CC EXTRACELLULAR DOMAIN TRIGGERS THE PROTEIN KINASE ACTIVITY OF THE
CC CYTOPLASMIC DOMAIN.
CC -I- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: PREDOMINANTLY IN THE PISTIL AND ANTHER.
CC -I- POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN
CC B.OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
CC -I- SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
CC GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
CC A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
CC -----
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CC -----
DR EMBL: M76647; AAA33000.1; ALT_TERM.
DR InterPro: IPR001480; B_lectin.
DR InterPro: IPR000719; Euk-pxkinase.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR004040; Sry_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000858; Slocus_glycop.
DR Pfam: PF000069; kinase.1.
DR Pfam: PF00954; Slocus_glycop.1.
DR Pfam: PF01453; Agglutinin.1.
DR

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097d61
ID 097d61 PRELIMINARY: PRT: 217 AA.
AC 097d61:
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Amino acid ABC transporter, permease component.
CN CAC3619.
OS Clostridium acetobutylicum.
OC Bacteria: Firmicutes: Bacillus/Clostridium group: Clostridia:
OC Clostridiales: Clostridiaceae: Clostridium.
OX NCB1_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA Tatusov R.L., Sabahe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007858; AAK81542.1; -
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp; 1.
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBR; 1.
KW Complete proteome.
SQ SEQUENCE 217 AA: 23743 MW: 36738BCDCDE8A2F CRC64:

Query Match 9.2%; Score 88.5; DB 16; Length 217;
Best Local Similarity 24.8%; Pred. No. 0.25;
Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

QY 16 SLIAACIPQLRCSSNTPPLTCQRCNASY-----TNSKGNAT----LMTCLGL 62
DB 4 SSIINKYIPVLLDGRITLLTLCSSIIIGCIITIAMFTSSVKVNLIGKFTWLKGT 63
QY 63 SLIISIAVFF--LMFLLRKISSEPLKDEF-----KNTGS-----GLIGMANIDLEKSR 108
DB 64 PLILQILVYVYIGLPISDKLITMPKAAIIGLSLNSGAVIAETIRGGIILADNGQEFASK 123
QY 109 -----TGDEIILPRGLEYVEEC-----TCEDCI-KSRPKVDSH 142
DB 124 ALGLTGGTMRKRIIPQAIRVIVIPCGNERFIAMIKDTSLSVITMBELKKAQLLVSSSG 183
QY 143 CFPLEPMESGA--TIVVTTNDYCKSLPAALSATELEKIS 182
DB 184 DAVTPYLFAGIFYLITLTITFTGIFSK-----IEKKLS 215
RESULT 3
Q8R056 PRELIMINARY: PRT: 842 AA.
ID Q8R056:
AC Q8R056:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Hypothetical 94.5 kDa protein.
OS Mus musculus (mouse).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sclurognathi: Muridae: Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028286; AAH28286.1; -
KW Hypothetical protein.
SQ SEQUENCE 842 AA: 94478 MW: 734C10D715E5BC92 CRC64:

Query Match 9.0%; Score 86.5; DB 11; Length 842;

Best Local Similarity 22.7%; Pred. No. 1.9;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
QY 18 LNAICIPQLRCSSNTPPLTCQRCNASYNSVGTAAIIMTCLGLISLAVFVLPFL 77
DB 126 LVGCFFCMCR-----CNK-CGGMOROKONAPCRRKCLGLVLCILMSIGITV 176
QY 78 RKISSEPLKDEFKNTSGSLIGMANIDLEKSRGD-EIIL--PRGLETVVEECTCE---- 129
DB 177 GFANQOTRRIRIKGTOK-----LAKSNRPDTLLTETPKQIDYVEQYTNKNKA 227
QY 130 ---DCIKS-----KPKVSDHCFFPLPAMEGATILVTK--TNDYCKSLPAL-- 172
DB 228 FSDLDIGSVLGRIRKQDKPKV-----TPVLEEKAMATAIKOTKDALQWSSSLKS 280
QY 173 ---SATEIEKISIA 183
DB 281 LDPAATQNLNTNLS 294

RESULT 4

Q9Y1X8 PRELIMINARY: PRT: 1193 AA.
ID Q9Y1X8:
AC Q9Y1X8:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Protein tyrosine kinase.
GN EPPK178.
OS Ephydatia fluviatilis.
OC Eukaryota: Metazoa: Porifera: Demospongiae: Ceractinomorpha;
OC Haplosclerida: Spongillidae: Ephydatia.
OX NCB1_TaxID=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9246375; PubMed=10229568;
RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA Miyata T.;
RT "Extensive gene duplication in the early evolution of animals before
RT the parazoan-eumetazoan split demonstrated by g proteins and protein
RL tyrosine kinases from sponge and hydra.";
RL J. Mol. Evol. 48:646-653(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21601119; PubMed=11738833;
RA Suga H., Katoh K., Miyata T.;
RT "Sponge homologs of vertebrate protein tyrosine kinases and frequent
RT domain shufflings in the early evolution of animals before the
RT parazoan-eumetazoan split.";
RL Gene 280:195-201(2001).
DR EMBL: AB006570; BAA81724.2; -
DR HSSP: P08631; 1AD5.
DR InterPro: IPR000494; EGFR_L_domain.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001368; TNFR_c6.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF01030; Recep_L_domain; 2.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 2.
DR SMART: SM00261; FU_6.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 1193 AA: 128169 MW: 009E4AC9BC12DF60 CRC64:

Query Match 8.9%; Score 85.5; DB 5; Length 1193;
 Best Local Similarity 22.3%; Pred. No. 3.6;
 Matches 37; Conservative 28; Mismatches 56; Indels 45; Gaps 8;

OY 2 LOMAGCCSNEFRBLSLHACIPQLRCSSTNP-----LTCQRYCNASVTNSVKGITNAIL 56
 DB 715 LCVSGCGSNDTEYODALN-CLPCNAGCICGSGPSISQCLTCA--SGSCITTDVQSSGCI 771
 OY 57 WVCGLSLIISLA---VFVLMFLRKISSEPLKDEKFNCGSLGMANIDLEKSRGDEI 113
 DB 772 GIVFGSIVVIFLATSTVLFLYRREYRKHNRQSTQST--WCYSN-----GNET 820

OY 114 ILPRGLEVEVECTCEDCIKSKPKVSDH---CFPLPAMEEGATI 155
 DB 821 LRP-----PKLRPPDNRRLITPELTALEGGQVL 847

RESULT 5
 O8RWV7 PRELIMINARY; PRT; 938 AA.

AC O8RWV7: 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 103.6 kDa protein.
 GN AT3648195.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID-3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Yamada K., Bann J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carinaci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamaya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen P., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shimozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RT "Arabidopsis Full length cDNA Clones";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY091078; AAM13898.1;
 KW Hypothetical protein.
 SQ SEQUENCE 938 AA; 103602 MW; 3E78395D65D75C95 CRC64;

Query Match 8.7%; Score 83.5; DB 10; Length 938;
 Best Local Similarity 29.4%; Pred. No. 4.5;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

OY 38 QRCNMSVTNSVKGITNAILMTCLGLSLISLAVFLMFLRKISSEPLKDEKRN--TGS 94
 DB 29 ERYCSA---NSALGTPSM--C-----SSTGPFQDSSEFENSLGP 62

OY 95 GLGGMANIDLEKSRGDEILPRGLEVEVECTCEDCIKSKP-----KYVSDHCFLPAM 149
 DB 63 SLVKLSLDM--SRLDG-----RGHFFDEGSGCNGRSSAPGLNTGNVDMCGDL--M 113

OY 150 EGCATT 155
 DB 114 DGCATT 119

RESULT 6
 O9STR8 PRELIMINARY; PRT; 1998 AA.

AC O9STR8: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Hypothetical 223.5 kDa protein.
 GN T24C20_80.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID-3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Choinske N., Robert C., Brothier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.,
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL096856; CAB31067.1;
 DR InterPro: IPR000515; BPD_transp.
 DR InterPro: IPR001683; PX.
 DR Pfam: PF00787; PX; 1.
 DR SMART: SM00312; PX; 1.
 DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1998 AA; 223513 MW; 8B3D6A03CD248F55 CRC64;

Query Match 8.7%; Score 83.5; DB 10; Length 1998;
 Best Local Similarity 29.4%; Pred. No. 11;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

OY 38 QRCNMSVTNSVKGITNAILMTCLGLSLISLAVFLMFLRKISSEPLKDEKRN--TGS 94
 DB 1089 ERYCSA---NSALGTPSM--C-----SSTGPFQDSSEFENSLGP 1122

OY 95 GLGGMANIDLEKSRGDEILPRGLEVEVECTCEDCIKSKP-----KYVSDHCFLPAM 149
 DB 1123 SLVKLSLDM--SRLDG-----RGHFFDEGSGCNGRSSAPGLNTGNVDMCGDL--M 1173

OY 150 EGCATT 155
 DB 1174 DGCATT 1179

RESULT 7
 O97491 PRELIMINARY; PRT; 327 AA.

AC O97491: 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Fas protein.
 GN FAS.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID-9940;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOCTE;
 RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
 RT "Cloning of sheep fas antigen";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB011671; BAA37093.1;
 DR HSSP: P25445; 1DDF
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 327 AA; 36928 MW; 5CFEB844B2B387A CRC64;

Query Match 8.5%; Score 82; DB 6; Length 327;
 Best Local Similarity 23.0%; Pred. No. 1.9;
 Matches 54; Conservative 25; Mismatches 68; Indels 88; Gaps 15;

QY 8 CSQ-NEFDSLHIA--CIPQL-----RCSN-----T 32
 DB 84 CSEGETYDMSHSDKIRSCVDEHGLEVEHNRCTONTKCRCKSNFPCNSPCEHCN 143
 QY 33 PPLTCO---RYCNASVATNSVKG---TNALIMTCLGLSLISLAVFLMLRK----- 79
 DB 144 PCTTCCEGIIKCTPTPSNTCKGSRHTNS-LNALILILILIFLITVYVRRRRRKNK 202
 QY 80 ---ISSEPLDEKRNKSGLLGMANIDLKSRG-----DEILPRGLEVTVEEC 126
 DB 203 NGKCVSAASDEGRQ-----LNLTDVLDGKYIPISIAELMKITEKFEVRKNGM---EEA 253
 QY 127 TCEDCIKSRKRVSDHCFPLPAMEGATIL-----VTKINDY--KSLPALIS 173
 DB 254 KIDIMH-----DNLH---ETAOKVQLLRKMYQSHGKNAYCTLTKNLPKALA 299

RESULT 8

QBYEV6 PRELIMINARY; PRT; 314 AA.
 AC QBYEV6;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Olfactory receptor MOR202-36.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitt. (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A073792; AAL6145.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 34996 MW; 9C7B11A5917EA632 CRC64;

Query Match 8.5%; Score 81.5; DB 11; Length 314;
 Best Local Similarity 30.4%; Pred. No. 2.1;
 Matches 31; Conservative 16; Mismatches 40; Indels 15; Gaps 6;

QY 8 CSQNEFDSLHACIP-COLRCSSNT-----PPLTCORYCNASVATNSVKGNTALMT 58
 DB 146 CYMGIGLOSSIHVALACFLSCNSNVNHFCDLPL-LDISCDVTYNEI--TVLLGT 202
 QY 59 CIG-LSLITSLAVFLMF--LKRISSEPLKDEKNTGSL 97
 DB 203 CDGILTLVLITNYLLIFAILRMSAEQRKAFSTCASHLI 244

RESULT 9

Q94711 PRELIMINARY; PRT; 2233 AA.
 AC Q94711;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE 51C surface protein.
 OS Parametium tetraurelia.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillida;
 OC Parametium.
 RN NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92106337; PubMed=1762150;
 RA Nielsen E., You Y., Forney J.;
 RT "Cysteine residue periodicity is a conserved structural feature of
 RT variable surface proteins from Parametium tetraurelia."
 RL J. Mol. Biol. 222:835-841(1991).
 DR EMBL: M65164; AAA61740.1;
 DR InterPro: IPR002895; Parametium_SA.
 DR Pfam: PF01508; Parametium_SA; 25.
 SQ SEQUENCE 2233 AA; 237078 MW; C064FE0AF7BB873B CRC64;

Query Match 8.5%; Score 81.5; DB 5; Length 2233;
 Best Local Similarity 25.1%; Pred. No. 20;
 Matches 43; Conservative 17; Mismatches 58; Indels 53; Gaps 10;

QY 6 GQCSQNEFDSLHACIPCOLRCSSNTPPLTCORYCNA-SVTSVKTNAILMTCLGLSL 64
 DB 520 GSCYQKQ-----CSAASQDNTTHAQCEYLPACTLSMTKKG-----CIDLPL 561
 QY 65 TISLAVFLMLRKISSEPLKDEKNTGSLGMANIDL-----EKSTODEIILPRGLE 120
 DB 562 TCSEA-----LVKENCELKANREK---CGWGSTCVDIVCTTAPKTTD-----D 603
 QY 121 YTVEECTC---EDCIKSRKRVSDHCFPLPAMEGATIL-----LVTTKN 162
 DB 604 YTVELCEAYKPPSSNCV---PNGTRKGMELAJACESHTIKQCDVACTKTN 651

RESULT 10

Q39191 PRELIMINARY; PRT; 595 AA.
 AC Q39191;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Serine threonine kinase.
 GN PRO25.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RN NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=93066369; PubMed=1438303;
 RA Smith T.A., Kohorn B.D.;
 RT "An Arabidopsis serine threonine kinase homologue with an EGF repeat
 RT selected in yeast for its specificity for a thylakoid membrane
 RT protein."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10989-10992(1992).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: L04999; AAA32844.1;
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD0000001; Euk_pkinase; 1.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Kinase;
 KW Repeat; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 595 AA; 65899 MW; 7B58FC1A656E0641 CRC64;
 Query Match 8.4%; Score 81; DB 10; Length 595;
 Best Local Similarity 24.5%; Pred. No. 4.9;
 Matches 39; Conservative 27; Mismatches 49; Indels 44; Gaps 10;

QY 8 CSONEFYDLSLHACIPCO--LRCSN-----TPPLTCOR-----YCNA-----SV 45
 DB 127 CRNCEGFDGPIYLSAGCDVNECTSTSIHRHNSDPTKRNKVGFCYCKGSGYRLDTT 186
 QY 46 TNSVK-----GTNAIILMTCLSLIISLAVVLMFLRKISSEPLKDE-FKNTGSGLL-- 97
 DB 187 TMSCKRKEFAWTTILLVTTIGF-LVILIGVACIOQRMKHLKDKTRLEQFEONGGMLTQ 245
 QY 98 ---GMANID-----LEKSRGT--DEILPRGLETV 123
 DB 246 RLSPSNVWDKIFTEDEGMRKATNGAYASRILGGGGQTV 284

RESULT 11
 ID 001892 PRELIMINARY; PRT; 773 AA.
 AC 001892;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE R08F11.7 protein.
 GN R08F11.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitoidea;
 OC Rhabdilitidae; Peloderiinae; Caenorhabditis.
 NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MEDLINE=99069613; PubMed=9851916;
 RX None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Minx P.;
 RT "The sequence of C. elegans cosmid R08F11.";
 RN [3]
 RP Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RA SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003385; AAB54249.1; -;
 DR HSSP: P05164; ICPX.
 DR InterPro: IPR002007; Anim_peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 SQ SEQUENCE 773 AA; 83992 MW; 4E3373FPA4EC67C7 CRC64;

Query Match 8.4%; Score 81; DB 5; Length 773;
 Best Local Similarity 21.7%; Pred. No. 6.6;
 Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6;

QY 177 IERS 180
 DB 362 IDON 365

RESULT 12
 ID 081820 PRELIMINARY; PRT; 735 AA.
 AC 081820;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE wall-associated kinase 1 (putative wall-associated kinase 1).
 GN WAK1 OR F16F4.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99308512; PubMed=10380805;
 RA He Z.H., Cheeseman I., He D., Kohorn B.D.;
 RT "A cluster of five cell wall associated receptor kinase genes, WAK1-5,
 RT are expressed in specific organs of Arabidopsis.";
 RL Plant Mol. Biol. 39:1189-1196(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
 RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,
 RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamita A.,
 RA Karlin-Neumann G., Kawai J., Kim C., Koeseema E., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinozaki K., Southwick A., Tracy S.E.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene F16F4.6 (GI:8920634)."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ009696; CAN08794.1; -;
 DR EMBL: AY039917; AAK64021.1; -;
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR InterPro: IPR004040; STY_Pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Prodom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00221; STYK; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; kinase;
 KW Repeat; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 735 AA; 81211 MW; AAD41A28296093B6 CRC64;

Query Match 8.3%; Score 80; DB 10; Length 735;
 Best Local Similarity 24.2%; Pred. No. 8;
 Matches 39; Conservative 27; Mismatches 49; Indels 46; Gaps 10;

QY 8 CSONEFYDLSLHACIPCO--LRCSN-----TPPLTCOR-----YCNA-----SV 45
 DB 264 CRNCEGFDGPIYLSAGCDVNECTSTSIHRHNSDPTKRNKVGFCYCKGSGYRLDTT 323
 QY 46 TNSVK-----GTNAIILMTCLSLIISLAVVLMFLRKISSEPLKDE-FKNTGSGLL-- 97
 DB 324 TMSCKRKEFAWTTILLVTTIGF-LVILIGVACIOQRMKHLKDKTRLEQFEONGGMLTQ 382

QY 98 -----GMANID-----LEKSRG--DEILPRGLETV 123
 DB 383 RLSGAGPSNVDKLTFEDGMRKATNGYAESRLDGGCGGTV 423

RESULT 13

Q26489 PRELIMINARY: PRT: 1299 AA.
 Q26489;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_Taxid=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SP9;
 RA Clepik M., Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 frugiperda (sf9) cells."; to the EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 268888; CAA93116.1; -.
 DR HSSP; Q99405; IMPT.
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR002099; Peptidase_S8.
 DR InterPro: IPR002884; P_domain.
 DR Pfam; PF01483; F; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR Prodom; PD000717; P_domain; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Peptidase.
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BHC572AB CRC64;

Query Match 8.2%; Score 79.5; DB 5; Length 1299;
 Best Local Similarity 24.1%; Pred. No. 17;
 Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEYFDLSLHACIPCOLRCS-----SNTPLTCQRYCNAS-----VTNSYKGTNAL-W 57
 DB 1150 CSRRLRLDRLNQCVPC---CSERGYNSTPTDC-CHCNFENGECTINSSVAGKRRIAEW 1205
 QY 58 TGLGLS-----LIIISLAV-----FVLMFLRKISSEPLKDEKNTGSGLLGMAN 101
 DB 1206 GALTASADAPSVAVVTIYVCAAAVGLFTVLVLAQHSRPRKTKRTSVRG----- 1259
 QY 102 IDELEKSRGTDEILPR-GLETYVECTCEDCIKSPKVDSDH 142
 DB 1260 --VEYSR-----LPRTVDVDTV---LTSCDQEGPEYEH 1289

RESULT 14

Q8VFWO PRELIMINARY: PRT: 314 AA.
 Q8VFWO;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Olfactory receptor MOR202-16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073405; AAL61068.1; -.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 34987 MW; DE5CDDF63E382F8D CRC64;

Query Match 8.1%; Score 78.5; DB 11; Length 314;
 Best Local Similarity 30.4%; Pred. No. 4.4;
 Matches 31; Conservative 15; Mismatches 41; Indels 15; Gaps 6;

QY 8 CSQNEYFDLSLHACIP-COLRCSNT-----PPLTCQRYCNASVTNSYKGTNALMT 58
 DB 146 CYMGCILOSSHVALAFCLSCNSNVINHFRCDIPPL-LDISCSDTYNEI--IVLLIGT 202
 QY 59 CLG-LSLIISLAVFVLMF--LLRKISSEPLKDEKNTGSGLL 97
 DB 203 CDGILTLVLIINTYLLIFAILRMRSVEAQRKAFSTCASHLI 244

RESULT 15

Q9H677 PRELIMINARY: PRT: 485 AA.
 Q9H677;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CDNA: FLJ22531 f1s, clone HRC12890.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK026184; BAB15387.1; -.
 SQ SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;

Query Match 8.1%; Score 78.5; DB 4; Length 485;
 Best Local Similarity 26.3%; Pred. No. 7.2;
 Matches 35; Conservative 17; Mismatches 48; Indels 33; Gaps 6;

QY 47 NSVKGTAAILMTCLGLSLIISLAVFVLMFLRKISSEPLKDEFKNTG-----GLIGM 99
 DB 185 NRISSVSIFLYGPLGLPILS-----TWGQPMTFEFKQTSLSVDMKKVHLCMI 232
 QY 100 ANIDLEKSRGTDEILPRGLETYVECTCEDCIKSPK-----VDSHCPLPAME 150
 DB 233 PNLDLNDR--DIVLP-DVSQVSESSDEDSQTMWDPOGOTLLFLFVDFHSAPPYOOME 288
 QY 151 -EGATILVTTKTN 162
 DB 289 IWGVYTLTLTHLN 301

Search completed: November 12, 2002, 17:00:18
 Job time : 59.0687 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:48:46 : Search time 2.67382 Seconds

(without alignments)
346.847 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36
Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	181	23	Human B-cell matur
2	36	100.0	184	21	Amino acid sequenc
3	36	100.0	184	21	Human BCMA protei
4	36	100.0	184	22	Human BCMA protei
5	36	100.0	184	22	Human BCMA protei
6	36	100.0	184	22	Human BAF7 recepto
7	36	100.0	184	22	Human BAF7 recepto
8	36	100.0	184	22	Human BCMA recepto
9	32	88.9	521	20	Enterococcus faeca
10	32	88.9	521	23	E faecalis EF017 a

11	32	88.9	542	20	AAV00040
12	32	88.9	542	23	ABP43259
13	32	88.9	969	22	ABG28063
14	32	88.9	1118	22	ABB62925
15	31	86.1	281	21	AA621219
16	31	86.1	294	21	AA621218
17	31	86.1	639	22	AAU33894
18	31	86.1	646	22	AAU36711
19	30	83.3	166	16	AAU71259
20	30	83.3	193	6	AAU50343
21	30	83.3	344	21	AAU31132
22	30	83.3	369	21	AAU31131
23	30	83.3	369	21	AAU39949
24	30	83.3	394	21	AAU39947
25	30	83.3	401	22	AAU39947
26	30	83.3	439	22	AAU39947
27	30	83.3	450	21	AAU39947
28	30	83.3	456	22	AAU39947
29	30	83.3	475	21	AAU39947
30	30	83.3	526	22	AAU39947
31	30	83.3	526	23	AAU76340
32	30	83.3	526	23	AAU76341
33	30	83.3	766	20	AAU00870
34	30	83.3	1165	23	ABP26712
35	30	83.3	1174	23	ABP26712
36	29	80.6	161	22	AAU43223
37	29	80.6	252	22	ABB60972
38	29	80.6	623	22	ABB61371
39	28	77.8	50	22	ABB37396
40	28	77.8	50	22	ABB22692
41	28	77.8	50	22	AAU70525
42	28	77.8	50	23	AAU40174
43	28	77.8	114	21	AAU57045
44	28	77.8	146	21	AAU57044
45	28	77.8	165	21	AAU20000

ALIGNMENTS

RESULT 1	AAE15484	standard; Protein; 181 AA.
ID	AAE15484	
AC	AAE15484	
XX		
DT	12-MAR-2002	(first entry)
XX		
DE	Human B-cell maturation (BCMA) protein.	
XX		
KW	Human: transmembrane activator and intracellular CAML interactor; TACI.	
KW	Cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;	
KW	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;	
KW	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;	
KW	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;	
KW	Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;	
KW	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;	
KW	rheumatoid arthritis; atherosclerosis.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Region	5..38
FT		/note="Cysteine-rich consensus region; This is region
FT		is specifically claimed as SEQ ID NO: 7 in claim 1 of
FT	Domain	52..72
FT		/label="Transmembrane_domain
XX		
PN	WO200187979-A2.	
XX		
PD	22-NOV-2001.	
XX		

PF 14-MAY-2001; 2001MO-US15567.
 XX
 XX 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 DR WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand Interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure; Fig 10A; 94pp; English.
 CC The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML Interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein.
 XX
 SQ Sequence 181 AA:
 QY
 Db 102 EKSRTGD 108
 Query Match 100.0%; Score 36; DB 23; Length 181;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 Db 102 EKSRTGD 108
 RESULT 2
 AAB08843
 ID AAB08843 standard; peptide; 184 AA.
 XX
 AC AAB08843:
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of human.
 XX
 KW BCMA: necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 57..77
 XX /note="putative transmembrane domain"
 PN WO2000050633-A1.
 XX
 PD 31-AUG-2000.

XX
 PF 24-FEB-2000; 2000MO-US04925.
 XX
 XX 24-FEB-1999; 99US-0121485.
 PR
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Seed B, Ting A;
 DR WPI; 2000-558405/51.
 XX
 PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression -
 XX
 PS Claim 32; Fig 7A; 53pp; English.
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)-kB activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,
 CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing.
 XX
 SQ Sequence 184 AA:
 QY
 Db 105 EKSRTGD 111
 Query Match 100.0%; Score 36; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 Db 105 EKSRTGD 111
 RESULT 3
 AAY94001
 ID AAY94001 standard; Protein; 184 AA.
 XX
 AC AAY94001:
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE A human BCMA protein, a B cell protein related to TAC1.
 XX
 KW Human; BR43x2; TAC1 receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-Interactor; tumor necrosis factor; TNF;
 KW zeta activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX
 OS Homo sapiens.
 XX
 PN WO200040716-A2.
 XX
 PD 13-JUL-2000.

XX	07-JAN-2000; 2000MO-US00396.
PF	
XX	PR 07-JAN-1999; 99US-0226533.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Gross JA, Xu W, Madden K, Yee DP;
XX	
DR	WPJ: 2000-452538/39.
DR	N-PsDB: AAA58559.
XX	
PT	Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
PT	renal disease, graft versus host disease, and inflammation, comprises
PT	administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX	
PS	Disclosure; Page 15z; 175pp; English.
XX	
CC	The present sequence represents a human BCMA protein, a B cell protein
CC	related to transmembrane activator and CAML-interactor (TACI) receptor.
CC	TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC	domains of BR43x2 (an isoform of TNF), TACI or BCMA (a related B cell
CC	protein) receptor contain a cysteine rich domain, and are used for
CC	inhibiting znf4 activity. znf4 is a TNF ligand. They may also be used
CC	for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC	with activated or resting B lymphocytes, effector T-cells, or with
CC	antibody production. The antibody production is associated with an
CC	autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC	gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
CC	and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC	asthma, bronchitis, emphysema, end stage renal failure,
CC	glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
CC	neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC	amyloidosis, moderating immune response, immunosuppression, graft
CC	rejection, graft versus host disease, inflammation, insulin dependent
CC	diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC	septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC	agonists or antagonists can be used to treat hypertension, renal artery
CC	stenosis, or occlusion, and cholesterol or renal emboli.
XX	
S0	Sequence 184 AA;
QY	1 EKSRTGD 7
Db	105 EKSRGTD 111
Query Match	100.0%; Score 36; DB 21; Length 184;
Best Local Similarity	100.0%; Pred. No. 5,7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 4	
AAE09241	
XX AAE09241 standard; Protein: 184 AA.	
XX AC AAE09241:	
XX XX 19-NOV-2001 (first entry)	
DE Human BCMA protein.	
KW Human; TNF; Tumour necrosis factor; TALL-1; APRIL; TNF receptor;	
KM TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;	
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;	
psoriasis.	
XX Homo sapiens.	
OS MOZ00160397-A1.	
XX 23-AUG-2001.	
PD 28-NOV-2000; 2000MO-US32378.	
PF	

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XX 16-FEB-2000; 2000US-0182938.
PR 22-AUG-2000; 2000US-0226986.
XX
XX (GENE ) GENENTECH INC.
PA
XX
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Masters SA, Pitti RM;
PI Yan M;
XX
XX WPI: 2001-541628/60.
DR N-PSDB; AAD15902.
XX
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists
PS
PS Example 2; Fig 2; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX e.g. TACI or BCMA. The method is useful for treating pathological
XX conditions or diseases associated with increased TALL-1 and APRIL
XX expression or activity. TALL-1 and APRIL antagonists are used to
XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX They are useful for treating a mammal suffering from cancer such
XX as leukaemia, lymphoma, myeloma, cancers of lung and colon and
XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX psoriasis and lupus erythematosus. The present sequence is human
XX BCMA protein.
SQ
SQ Sequence 184 AA;
XX
XX
XX Query Match 100.0%; Score 36; DB 22; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 5.7;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
XXXXX|
DB 105 EKSRTGD 111
XX
XX
XX RESULT 5
XX ID AAE00506
XX AC AAE00506; Protein; 184 AA.
XX DT 31-JUL-2001 (first entry)
XX DE Human B cell maturation protein (BCMA).
XX
XX Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytosolic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lymphoproliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF;
XX tumour necrosis factor; BCMA; B cell maturation protein.
XX
XX Homo sapiens.
XX OS
XX PN WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX 11-FEB-2000; 2000US-0181807.
XX 30-JUN-2000; 2000US-0215688.
XX

```

PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX
PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX WPI: 2001-266242/27.
DR N-PSDB; AAD03844.
XX
PT Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor
PT (APRIL-R) antagonist -
XX
XX
PS Claim 3; Fig 3A; 85pp; English.
XX
CC The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or
CC carcinoma. The method involves administering a composition comprising
CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred to as
CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (grave's
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC human immunodeficiency virus (HIV), and for treating, suppressing or
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is human APRIL-R also referred to as BCMA or
CC BCM protein.
XX
SQ Sequence 184 AA;
QY
Db 105 EKSRTGD 111

Query Match 100.0%; Score 36; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
| | | | |
Db 105 EKSRTGD 111

RESULT 6
AAB60698
ID AAB60698 standard; Protein: 184 AA.
XX
AC AAB60698;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human BAFf receptor (BAFf-R).
XX
KW Human BAFf receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour.
XX
OS Homo sapiens.
XX
PN WO200112812-A2.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-US22507.
XX

PR 17-AUG-1999; 99US-0149378.
PR 11-FEB-2000; 2000US-0181684.
PR 18-FEB-2000; 2000US-0183536.
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX WPI: 2001-202866/20.
DR N-PSDB; AAF59998.
XX
PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFf-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFf-R
PT antibody homolog -
XX
XX
PS Claim 20; Fig 1; 59pp; English.
XX
CC The invention relates to the use of a BAFf receptor (BAFf-R, also known
CC as BCMA) protein, or a BAFf-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFf-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFf-R, fusion proteins containing it, and BAFf-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFf-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFf-R
CC proteins or BAFf-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFf-R and BAFf, thereby inhibiting inflammation. Since BAFf-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFf-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents human BAFf-R.
XX
SQ Sequence 184 AA;
QY
Db 105 EKSRTGD 111

Query Match 100.0%; Score 36; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
| | | | |
Db 105 EKSRTGD 111

RESULT 7
AAV71979
ID AAV71979 standard; Protein: 184 AA.
XX
AC AAV71979;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human B cell maturation factor (BCMA) protein.
XX
KW Human: Tumour Necrosis Factor; TNF; immunosuppressant; TAIL-1;
KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX

OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 1..62
/Label= Extracellular_domain
PN WO200068378-A1.
PD 16-NOV-2000.
PF 05-MAY-2000; 2000WO-US12266.
PR 06-MAY-1999; 99US-0132892.
PR 01-MAY-2000; 2000US-0201012.
XX
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
PI Shu HS;
DR WPI: 2001-016094/02.
DR N-PSDB; AA002125.
XX
PT Isolated TALL-1 protein is used to identify compounds that regulate B
PT lymphocyte proliferation, used to treat B lymphocyte associated
PT autoimmune disorders -
XX
PS Claim 37: Page 104-105; 112pp; English.
XX
CC The present invention relates to Tumour necrosis factor (TNF) and
CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
CC molecules, proteins (including homologues), and their antibodies. The
CC invention in particular relates to methods for regulating the
CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC mediated immune responses. TALL-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
CC The TALL-1 protein and its corresponding nucleic acid sequence are also
CC useful in diagnostic assays.
CC The present sequence is a human B cell maturation factor (BCMA)
CC protein. It is the receptor for TALL-1 protein. BCMA gene is
CC located on chromosome 16. In human tissues, BCMA is expressed by
CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
CC lymphocyte stage but its expression increases with B lymphocyte
CC maturation.
XX
SQ Sequence 184 AA:
Query Match 100.0%; Score 36; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKSRTGD 7
Db 105 EKSRTGD 111
RESULT 8
ID ABB81487 standard; Protein: 184 AA.
XX
AC ABB81487;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human BCMA receptor related protein SEQ ID NO:7.
XX

KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antiabiotic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO200238766-A2.
PD 16-MAY-2002.
PF 05-NOV-2001; 2001WO-US47018.
PR 07-NOV-2000; 2000US-246449P.
PR 20-DEC-2000; 2000US-257131P.
PR 28-JUN-2001; 2001US-301715P.
PR 29-AUG-2001; 2001US-315565P.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Gross JA, Xu W, Henne RM, Grant FJ;
DR WPI: 2002-508212/54.
XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma -
XX
PS Disclosure: Page 135-136; 154pp; English.
XX
CC The present invention describes a human tumour necrosis factor receptor
CC designated ztnfr12 (1). (1) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antihemetic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (1) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12
CC (e.g. TNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (1) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (1) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is
CC given in the exemplification of the present invention.
XX
SQ Sequence 184 AA:
Query Match 100.0%; Score 36; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKSRTGD 7
Db 105 EKSRTGD 111
RESULT 9
AAAY00041

ID	AAV00041 standard; Protein; 521 AA.
XX	
AC	AAV00041;
XX	
DT	20-APR-1999 (first entry)
XX	
DE	Enterococcus faecalis antigenic polypeptide fragment EF017.
XX	
KW	Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
XX	detection; attenuation; antigenic.
XX	
OS	Enterococcus faecalis.
XX	
PN	WO9850554-A2.
XX	
PD	12-NOV-1998.
XX	
PE	04-MAY-1998; 98WO-US08959.
XX	
PR	14-NOV-1997; 97US-0066009.
XX	
PR	06-MAY-1997; 97US-0044031.
XX	
PR	16-MAY-1997; 97US-0046655.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Bailey C, Choi GH, Hromocky] A, Kunsch CA;
XX	
DR	WPI; 1999-070095/06.
DR	N-PSDB; AAX20031.
XX	
PT	New isolated Enterococcus faecalis polynucleotides - used to develop
PT	products for the detection of Enterococcus and for use in vaccines
PT	for prevention or attenuation of Enterococcus infection
XX	
PS	Claim 9; Page 96; 301pp: English.
XX	
CC	The present sequence represents an antigenic polypeptide fragment
CC	isolated from Enterococcus faecalis. The present invention describes
CC	genes, proteins and antigenic polypeptides isolated from E. faecalis.
CC	The proteins can be used in vaccines for preventing or attenuating an
CC	infection caused by a member of the Enterococcus genus in an animal.
CC	They can also be used for detecting Enterococcus antibodies in a sample.
CC	The nucleotide sequences can be used for detecting Enterococcus nucleic
CC	acids. Products from the present invention can also be used for
CC	screening compounds to identify agonists and antagonists of E. faecalis
CC	protein activity.
XX	
XX	
SO	Sequence 521 AA;
XX	
QY	1 EKSRTGD 7
XX	:
DB	405 EKSRTGD 411
XX	
RESULT 10	
ABP43260	
ID	ABP43260 standard; Protein; 521 AA.
XX	
AC	ABP43260;
XX	
DT	05-AUG-2002 (first entry)
XX	
DE	E faecalis EF017 antigenic fragment.
XX	
KW	Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic.
XX	
OS	Enterococcus faecalis.
XX	
PN	US2002045737-A1.

[illegible]

PT for prevention or attenuation of Enterococcus infection
XX
PS Claim 9: Page 95-96; 301pp; English.
XX

CC The present sequence represents a protein isolated from
CC Enterococcus faecalis. The present invention describes genes, proteins
CC and antigenic polypeptides isolated from E. faecalis. The proteins can
CC be used in vaccines for preventing or attenuating an infection caused
CC by a member of the Enterococcus genus in an animal. They can also be
CC used for detecting Enterococcus antibodies in a sample. The nucleotide
CC sequences can be used for detecting Enterococcus nucleic acids.
CC Products from the present invention can also be used for screening
CC compounds to identify agonists and antagonists of E. faecalis protein
CC activity.
XX

SO Sequence 542 AA;

Query Match 88.9%; Score 32; DB 20; Length 542;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EKSRTGD 7
||||:|
Db 426 EKSRSKD 432

RESULT 12

ID ABP43259 standard; Protein: 542 AA.

AC ABP43259;

DT 05-AUG-2002 (first entry)

DE E faecalis EF017 protein.

XX Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic.

OS Enterococcus faecalis.

PM US2002045737-A1.

PD 18-APR-2002.

PF 04-MAY-1998; 98US-0071035.

PR 04-MAY-1998; 98US-0071035.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Choi GH, Bailey C, Hromocky A, Kunsch CA;

DR WPI: 2002-425450/45.

DR N-PSDB; ABR98015.

PT New genes and polypeptides from Enterococcus faecalis, useful as
PT vaccines for preventing, treating or attenuating an infection caused by
PT a member of the Enterococcus genus in an animal, particularly E.
PT faecalis -

PS Claim 9: Page 47; 255pp; English.

XX The present invention provides the protein and coding sequences of a
XX number of polypeptides from Enterococcus faecalis. The proteins can be
XX used as vaccines for preventing or attenuating an infection caused by a
XX member of the Enterococcus genus in an animal, particularly E. faecalis.
XX The polynucleotide is also useful for preventing or treating E. faecalis
XX infection. The present sequence is a protein of the invention.

SO Sequence 542 AA;

Query Match 88.9%; Score 32; DB 23; Length 542;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EKSRTGD 7
||||:|
Db 426 EKSRSKD 432

RESULT 13

ID ABG29063 standard; Protein: 969 AA.

AC ABG29063;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #29054.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PM WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS93250.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID No 59422; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 969 AA;

Query Match 88.9%; Score 32; DB 22; Length 969;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db	463	KKSRTGD 469
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XX	AC	ABB62925;
XX	DT	26-MAR-2002 (first entry)
DE	XX	Drosophila melanogaster polypeptide SEQ ID NO 15567.
XX	XX	Drosophila developmental biology; cell signalling; insecticide;
KW	XX	pharmaceutical.
OS	XX	Drosophila melanogaster.
XX	PN	WO200171042-A2.
XX	PD	27-SEP-2001.
XX	PR	23-MAR-2001; 2001WO-US09231.
PF	XX	23-MAR-2000; 2000US-191637P.
PR	XX	11-JUL-2000; 2000US-0614150.
PA	(PEKE)	PE CORP NY.
PI	Venter JC,	Adams M, LI PWD, Myers EW;
DR	N-PDB:	ABL07028.
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	
PS	Disclosure:	SEQ ID NO 15567; 21pp + Sequence Listing; English.
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-AB572072).	
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
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Query Match	Best Local Similarity	88.9%; Score 32; DB 22; Length 1118;
Matches	6; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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Db	966	EKDRTGD 992
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XX	AC	AAG21219;
XX	DT	17-OCT-2000 (first entry)

DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23696.
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KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
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OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
FE	25-FEB-2000; 2000EP-0301439.
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PR	19-APR-1999; 99US-0130077.
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PR	23-APR-1999; 99US-0130510.
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PR	28-APR-1999; 99US-0131449.
PR	30-APR-1999; 99US-0132048.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 85.7%; Pred. NO. 1e+02; 1; Indels 0; Caps 0;
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Qy 1 EKSRGCD 7
Db 212 EKSRVCD 218

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Job time : 3.67382 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

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214.236 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111
Perfect score: 36
Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	32	88.9	542	4	US-09-071-035-62	Sequence 62, App1
3	30	83.3	766	4	US-09-463-238-6	Sequence 6, App1
4	28	77.8	288	2	US-08-424-641B-11	Sequence 11, App1
5	28	77.8	288	2	US-08-820-980-11	Sequence 11, App1
6	28	77.8	288	2	US-08-826-439-11	Sequence 11, App1
7	27	75.0	55	4	US-09-227-357-553	Sequence 553, App
8	27	75.0	77	4	US-09-227-357-552	Sequence 552, App
9	27	75.0	174	4	US-08-683-262B-42	Sequence 42, App1
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11	27	75.0	190	2	US-08-462-481-5	Sequence 5, App1
12	27	75.0	190	2	US-08-436-771-7	Sequence 7, App1
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14	27	75.0	190	2	US-08-487-797-7	Sequence 7, App1
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18	27	75.0	344	3	US-08-733-837B-6	Sequence 6, App1
19	27	75.0	371	2	US-08-378-617A-12	Sequence 12, App1
20	27	75.0	394	1	US-07-914-281-4	Sequence 4, App1
21	27	75.0	394	1	US-08-393-246-4	Sequence 4, App1
22	27	75.0	394	1	US-08-525-058A-4	Sequence 4, App1
23	27	75.0	394	2	US-08-696-731-4	Sequence 4, App1
24	27	75.0	394	4	US-09-042-531-4	Sequence 4, App1
25	27	75.0	394	4	US-08-379-040-2	Sequence 2, App1
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27	27	75.0	476	3	US-09-188-579-114	Sequence 114, App

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29	27	75.0	476	4	US-09-134-218-6	Sequence 6, App1
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31	27	75.0	590	4	US-09-232-191-25	Sequence 25, App1
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35	27	75.0	650	4	US-09-232-191-29	Sequence 29, App1
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37	27	75.0	650	4	US-09-232-200-97	Sequence 97, App1
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41	27	75.0	650	4	US-09-232-201-97	Sequence 97, App1
42	27	75.0	1288	3	US-08-762-428A-6	Sequence 6, App1
43	26	72.2	14	6	5164485-4	Patent No. 5164485
44	26	72.2	19	4	US-08-818-112-56	Sequence 56, App1
45	26	72.2	19	4	US-08-818-112-122	Sequence 122, App

ALIGNMENTS

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RESULT 1
US-09-071-035-64
: Sequence 64, Application US/09071035
: Patent No. 6448043
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: GENERAL INFORMATION:
: APPLICANT: GIL H. Choi
: TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071,035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brookes
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 64:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 521 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
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: US-09-071-035-64
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: Query Match 88.9% Score 32: DB 4: Length 521:
: Best Local Similarity 85.7% Pred. No. 29:
: Matches 6: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
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: Db 405 EKSRSRD 411
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RESULT 2
US-09-071-035-62
: Sequence 62, Application US/09071035
: Patent No. 6448043
: GENERAL INFORMATION:
: APPLICANT: Gil H. Choi
: TITLE OF INVENTION: Enterococcus faecalis polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 Inch, 1.4Mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071,035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brooks
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 542 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-071-035-62

Query Match      .      88.9%; Score 32; DB 4; Length 542;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      426 EKSRSGD 432

RESULT 3
US-09-463-238-6
: Sequence 6, Application US/09463238
: Patent No. 6469230
: GENERAL INFORMATION:
: APPLICANT: Edwards, Elizabeth A
: APPLICANT: Smith, Alison M
: APPLICANT: Bustos Gullen, Regla
: APPLICANT: Martin, Catherine R
: APPLICANT: Plant Bioscience Limited
: TITLE OF INVENTION: Starch Debranching Enzymes
: FILE REFERENCE: 97,118
: CURRENT APPLICATION NUMBER: US/09/463,238
: CURRENT FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: PCT/GB98/02280
: PRIOR FILING DATE: 1998-07-30
: PRIOR APPLICATION NUMBER: GB 9716185.5
: PRIOR FILING DATE: 1997-07-31
: NUMBER OF SEQ ID NOS: 30
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: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 766
: TYPE: PRT
: ORGANISM: Solanum tuberosum
: US-09-463-238-6

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Best Local Similarity 71.4%; Pred. No. 1.1e+02;
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Db      141 QKNRTGD 147

RESULT 4
US-08-424-641B-11
: Sequence 11, Application US/08424641B
: Patent No. 5824523
: GENERAL INFORMATION:
: APPLICANT: Sylvain Moineau, Shirley A.
: APPLICANT: Walker, Enezer R. Vedamuthu,
: APPLICANT: and Peter A. Vandenberg
: TITLE OF INVENTION: Isolated DNA Encoding
: TITLE OF INVENTION: Enzyme For Phage
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ian C. McLeod
: STREET: 2190 Commons Parkway
: CITY: Okemos
: STATE: Michigan
: COUNTRY: USA
: ZIP: 48864
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
: MEDIUM TYPE: storage
: COMPUTER: Acer
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/424,641B
: FILING DATE: April 19, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/366,480
: FILING DATE: December 30, 1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ian C. McLeod
: REGISTRATION NUMBER: 20,931
: REFERENCE/DOCKET NUMBER: MT 4.1-151
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (517) 347-4100
: TELEFAX: (517) 347-4103
: TELEEX: NO. 5824523e
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 288 Amino Acids
: TYPE: Amino Acid
: STRANDEDNESS: Single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
: US-08-424-641B-11

Query Match      77.8%; Score 28; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      144 KNRTGD 149
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RESULT 5
US-08-820-980-11
Sequence 11 Application US/08820980
Patent No. 5925388
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: Storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,980
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5925388e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-820-980-11

Query Match 77.8%; Score 28; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRIGD 7
1:|||||
DB 144 KNRTGD 149

RESULT 6
US-08-826-439-11
Sequence 11 Application US/08826439
Patent No. 5972673
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: Storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,439
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5972673e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-826-439-11

Query Match 77.8%; Score 28; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRIGD 7
1:|||||
DB 144 KNRTGD 149

RESULT 7
US-09-227-357-553
Sequence 553 Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08

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: EARLIER APPLICATION NUMBER: 60/051,932
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,916
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,930
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,918
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,920
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,733
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,795
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,919
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,928
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/055,722
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,723
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,948
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,949
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,953
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,950
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,947
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,964
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/056,360
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,684
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,984
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,954
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/058,785
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,664
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,660
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,661
: EARLIER FILING DATE: 1997-09-12
: NUMBER OF SEQ ID NOS: 672
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 553
: LENGTH: 55
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-227-357-553
Query Match      75.0%: Score 27: DB 4: Length 55:
Best Local Similarity 83.3%: Pred. No. 37:
Matches 5: Conservative 0: Mismatches 1: Indels 0: Caps 0:
OY      2 KSRGTG 7
      1 11111
Db      7 KDRGTG 12

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: TITLE OF INVENTION: 123 Human Secreted Proteins
: FILE REFERENCE: P2010P1
: CURRENT APPLICATION NUMBER: US/09/227,357
: CURRENT FILING DATE: 1999-01-08
: EARLIER APPLICATION NUMBER: PCT/US98/13684
: EARLIER FILING DATE: 1998-07-07
: EARLIER APPLICATION NUMBER: 60/051,926
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,793
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,925
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,929
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,803
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,732
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,931
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,932
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,916
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,930
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,918
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,920
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,733
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: EARLIER APPLICATION NUMBER: 60/052,795
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,919
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,928
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/055,722
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,723
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,916
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,930
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,918
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,920
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/052,733
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/052,795
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,919
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,928
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/051,928
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: EARLIER APPLICATION NUMBER: 60/055,722
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: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,953
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,950
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,947
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,964
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/056,360
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,684
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/058,785
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,664
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,660
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,661
: EARLIER FILING DATE: 1997-09-12
: NUMBER OF SEQ ID NOS: 672
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 552

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LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-227-357-552

Query Match 75.0%; Score 27; DB 4; Length 77;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 KSRTGD 7
Db 29 KDRGTGD 34

RESULT 9
US-08-683-262B-42
Sequence 42, Application US/08683262B
Patent No. 5929220
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,262B
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-262B-42
Query Match 75.0%; Score 27; DB 2; Length 174;
Best Local Similarity 83.3%; Pred. No. 1,2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KSRTGD 7
Db 165 ESRGTGD 170

RESULT 10
US-09-361-707-42
Sequence 42, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
Li, Jisu
Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-361-707-42
Query Match 75.0%; Score 27; DB 4; Length 174;
Best Local Similarity 83.3%; Pred. No. 1,2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KSRTGD 7
Db 165 ESRGTGD 170

RESULT 11
US-08-462-481-5
Sequence 5, Application US/08462481
Patent No. 5840577
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Aimin
TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5840577
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,481
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-481-5

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:111
DB 58 EKARTAD 64

RESULT 12
US-08-436-771-7
Sequence 7, Application US/08436771
Patent No. 5861300
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESS: Russell
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,771
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-771-7

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
11:111
DB 58 EKARTAD 64

RESULT 13
US-08-434-998-7
Sequence 7, Application US/08434998
Patent No. 5866781
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESS: Russell
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,998
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-998-7

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
11:111
DB 58 EKARTAD 64

RESULT 14
US-08-487-797-7
Sequence 7, Application US/08487797
Patent No. 5866787
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Holland & Knight
STREET: One E. Broward Boulevard, #1300
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,797
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/468-7811
TELEFAX: 305/463-2030
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-797-7

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:111
Db 58 EKARTAD 64

RESULT 15
US-08-701-005A-5
Sequence 5, Application US/08701005A
Patent No. 5877019
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Almin
TITLE OF INVENTION: Animal 2-5A-Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5877019
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 - 13th Street, N.W., Suite 701 E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,005A
FILING DATE: 21-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,304
FILING DATE: 22-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE//DOCKET NUMBER: N1255-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: E. coli
US-08-701-005A-5

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:111
Db 58 EKARTAD 64

Search completed: November 12, 2002, 17:01:41
Job time : 1.96137 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 17:00:26 : Search time 0.540773 Seconds
(without alignments)
186.640 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36
Sequence: 1 EKSRTGD 7

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Total number of hits satisfying chosen parameters: 92612

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PC1_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	181	10	US-09-854-864-5
2	31	86.1	639	10	US-09-815-242-5390
3	31	86.1	646	10	US-09-815-242-12304
4	28	77.8	50	10	US-09-864-761-37990
5	28	77.8	466	10	US-09-741-669-303
6	28	77.8	762	10	US-09-925-299-998
7	27	75.0	54	10	US-09-867-550-1596
8	27	75.0	144	10	US-09-815-242-11116
9	27	75.0	174	10	US-09-818-066-42
10	27	75.0	359	10	US-09-994-427A-11
11	27	75.0	382	10	US-09-825-414-30
12	27	75.0	394	10	US-09-863-475A-4
13	27	75.0	394	10	US-09-946-034-2
14	27	75.0	590	10	US-09-943-671-25
15	27	75.0	650	10	US-09-943-671-29
16	27	75.0	855	10	US-09-815-242-11930
17	27	75.0	2568	10	US-09-866-108-3
18	26	72.2	68	10	US-09-864-761-42165
19	26	72.2	68	10	US-09-864-761-46399

20 26 72.2 170 10 US-09-818-066-49
21 26 72.2 174 10 US-09-818-066-45
22 26 72.2 174 10 US-09-818-066-46
23 26 72.2 174 10 US-09-818-066-47
24 26 72.2 174 10 US-09-818-066-48
25 26 72.2 199 10 US-09-921-640-6
26 26 72.2 212 10 US-09-925-299-968
27 26 72.2 234 10 US-09-915-593-2
28 26 72.2 240 10 US-09-915-593-6
29 26 72.2 241 10 US-09-915-593-4
30 26 72.2 241 10 US-09-915-593-28
31 26 72.2 241 12 US-10-116-378-3
32 26 72.2 258 10 US-09-921-640-9
33 26 72.2 264 10 US-09-925-301-905
34 26 72.2 283 9 US-09-970-989-2
35 26 72.2 307 10 US-09-788-626-20
36 26 72.2 315 10 US-09-739-254-124
37 26 72.2 315 10 US-09-904-615-124
38 26 72.2 372 10 US-09-818-066-64
39 26 72.2 426 10 US-09-864-761-42921
40 26 72.2 469 10 US-09-925-300-1494
41 26 72.2 742 10 US-09-799-777-18
42 26 72.2 760 10 US-09-265-606-2
43 26 72.2 766 10 US-09-795-693-17
44 26 72.2 874 10 US-09-815-242-11809
45 26 72.2 876 10 US-09-815-242-10269

ALIGNMENTS

RESULT 1
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854, 864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204, 039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214, 591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0% Score 36; DB 10; Length 181;
Best Local Similarity 100.0% Pred. No. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
|||||||
DB 102 EKSRTGD 108

RESULT 2
US-09-815-242-5390
Sequence 5390, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlssen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel

```
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 5390
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5390
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Query Match      86.1%; Score 31; DB 10; Length 639;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 EKSRTGD 7
      1111111
DB      432 EKSNTGD 438
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RESULT 3
US-09-815-242-12304
; Sequence 12304, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12304
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12304
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Query Match      86.1%; Score 31; DB 10; Length 646;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 EKSRTGD 7
      1111111
DB      429 EKSNTGD 435
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RESULT 4
US-09-864-761-37990
; Sequence 37990, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 37990
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION: MAP TO AP000125.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65
OTHER INFORMATION: EST_HUMAN HIT: A0156079.1, EVALU0 2.20e+00
US-09-864-761-37990

Query Match 77.8%; Score 28; DB 10; Length 50;
Best Local Similarity 71.4%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
1:1111
DB 33 EKAHTGD 39

RESULT 5
US-09-741-669-303
Sequence 303, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Aliya
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
TITLE OF INVENTION: Proliferation of E. coli
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 466
TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-669-303

Query Match 77.8%; Score 28; DB 10; Length 466;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
1:1111
DB 194 ERSRAGD 200

RESULT 6
US-09-925-299-998
Sequence 998, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 998
LENGTH: 762
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-998

Query Match 77.8%; Score 28; DB 10; Length 762;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
1:1111
DB 9 EDSRTGD 15

RESULT 7
US-09-867-550-1596
Sequence 1596, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehran, Fuad.
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells a
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1596
LENGTH: 54
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-1596

Query Match 75.0%; Score 27; DB 10; Length 54;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTG 6
1:1111
DB 4 ERSRTG 9

RESULT 8
US-09-815-242-11116
Sequence 11116, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 11116
LENGTH: 144
TYPE: PR
ORGANISM: Hemophilus influenzae
US-09-815-242-11116

Query Match 75.0%; Score 27; DB 10; Length 144;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRGTG 6
:|||||
DB 38 QKSRGTG 43

RESULT 9

US-09-818-066-42
Sequence 42, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-818-066-42

Query Match 75.0%; Score 27; DB 10; Length 174;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRGTG 7
:|||||
DB 165 ESRGTG 170

RESULT 10
US-09-994-427A-11
Sequence 11, Application US/09994427A

Patent No. US20020128221A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Schieff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 11
LENGTH: 359
TYPE: PR
ORGANISM: Mus musculus
US-09-994-427A-11

Query Match 75.0%; Score 27; DB 10; Length 359;
Best Local Similarity 71.4%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKSRGTG 7
:|||||
DB 63 EKGRNGD 69

RESULT 11

US-09-825-414-30
Sequence 30, Application US/09825414
Patent No. US20020083489A1
GENERAL INFORMATION:
APPLICANT: Alfano, Alan
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 30
LENGTH: 382
TYPE: PR
ORGANISM: Pseudomonas syringae
US-09-825-414-30

Query Match 75.0%; Score 27; DB 10; Length 382;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKSRGTG 7
:|||||
DB 197 EKGRAGD 203

RESULT 12
US-09-863-475A-4
Sequence 4, Application US/09863475A
Patent No. US20020102688A1
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,475A
FILING DATE: 24-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,281
FILING DATE: 20-JUL-1992

ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 24885 OPAT UR

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-863-475A-4

Query Match
Best Local Similarity 71.4%; Score 27; DB 10; Length 394;
Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKSRGTD 7
11111
Db 98 EKRNGD 104

RESULT 13
US-09-946-034-2
Sequence 2, Application US/09946034
Patent No. US20020152486A1
GENERAL INFORMATION:
APPLICANT: Cooper, David K.C.
Koren, Eugen
TITLE OF INVENTION: GENETICALLY ENGINEERED ANIMALS FOR USE
AS ORGAN DONORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/946,034
FILING DATE: 04-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,817
FILING DATE: 20-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: BMC100

TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-946-034-2

Query Match
Best Local Similarity 71.4%; Score 27; DB 10; Length 394;
Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKSRGTD 7
11111
Db 98 EKRNGD 104

RESULT 14
US-09-943-671-25
Sequence 25, Application US/09943671
Patent No. US20020106733A1
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WH197-21P3ME
CURRENT APPLICATION NUMBER: US/09/943,671
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/232,191
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/093,491
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/110,941
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 590
TYPE: PRT
ORGANISM: Drosophila melanogaster

US-09-943-671-25

Query Match
Best Local Similarity 83.3%; Score 27; DB 10; Length 590;
Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 KSRGTD 7
11111
Db 450 KDRGTD 455

RESULT 15
US-09-943-671-29
Sequence 29, Application US/09943671
Patent No. US20020106733A1
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas

; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Fatty Acid Transport Proteins
; FILE REFERENCE: WHI97-21P3ME
; CURRENT APPLICATION NUMBER: US/09/943,671
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/232,191
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/093,491
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: 60/110,941
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-943-671-29

Query Match

75.0%; Score 27; DB 10; Length 650;

Best Local Similarity 83.3%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSRTGD 7

Db 505 KDRFGD 510

Search completed: November 12, 2002, 17:09:12
Job time: 1.54077 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:36 : Search time 1.08155 Seconds
(without alignments)
622.203 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36
Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	184	2 S43486	B-cell maturation
2	33	91.7	585	2 A69829	ABC transporter (A
3	32	88.9	862	2 A05028	IPQC protein homol
4	32	88.9	1163	2 S07137	DNA-directed RNA p
5	32	88.9	1361	2 A29959	DNA-directed RNA p
6	31	86.1	646	2 H89843	hypothetical prote
7	31	86.1	1195	2 E96615	hypothetical prote
8	30	83.3	92	2 AE3173	transcription regu
9	30	83.3	160	2 C97289	hypothetical prote
10	30	83.3	396	2 AH3650	glycosyl transfera
11	30	83.3	450	2 T04265	probable casein ki
12	30	83.3	463	2 E72268	astB/chur-related
13	30	83.3	526	2 S49641	L-galactonolactone
14	29	80.6	149	2 H70441	ribosomal protein
15	29	80.6	316	2 E95307	hypothetical prote
16	29	80.6	583	2 E83794	ABC transporter (A
17	29	80.6	1031	2 C81302	probable type I si
18	28	77.8	111	2 AG1906	photosystem II pr
19	28	77.8	115	2 B69188	nitrogen regulator
20	28	77.8	121	2 S19486	hypothetical prote
21	28	77.8	128	2 E70926	hypothetical prote
22	28	77.8	288	2 B24372	DpnII endonuclease
23	28	77.8	321	2 S35230	hype protein - Bra
24	28	77.8	324	2 AB2772	inosine-uridine pr
25	28	77.8	371	2 G84398	phosphate transpor
26	28	77.8	378	2 A97552	chain a, crystal s
27	28	77.8	412	2 S69633	hypothetical prote
28	28	77.8	415	2 AB3637	alpha-methylacyl-C
29	28	77.8	421	2 F83400	hypothetical prote

30	28	77.8	466	2 H64904	hypothetical prote
31	28	77.8	482	2 D90983	mannose-1-P guanos
32	28	77.8	482	2 G85828	mannose-1-P guanos
33	28	77.8	529	2 J00783	5S.3K sporulation
34	28	77.8	585	2 H83941	ABC transporter (A
35	28	77.8	589	2 H84985	hypothetical prote
36	28	77.8	600	2 S58681	selenocysteine trn
37	28	77.8	608	2 A53195	afamin precursor -
38	28	77.8	626	2 I38618	zinc finger protei
39	28	77.8	626	2 AF0358	conserved hypochet
40	28	77.8	645	2 T19382	hypothetical prote
41	28	77.8	727	1 A45995	copper-transportin
42	28	77.8	728	2 T36026	ABC excision nucle
43	28	77.8	761	2 T24230	hypothetical prote
44	28	77.8	832	2 S76815	hypothetical prote
45	28	77.8	1025	2 A82516	type I restriction

ALIGNMENTS

```
RESULT 1
S43486
B-cell maturation factor - human
N:Alternate names: BCM protein; BCMA protein; BEL protein
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C:Accession: S43486; S31208; S36651
R:Laabl, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapli, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bid
A:Reference number: S43486; MUID:94218235; PMID:8165126
A:Accession: S43486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LA4>
A:Cross-references: EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471245
R:Laabl, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapli
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the Interleukin 2 gene by a t(
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LA2>
A:Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:929408
A:Accession: S36651
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-184 <LA3>
A:Cross-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCMA
A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 44/1: 93/1
C:Superfamily: human B-cell maturation factor

Query Match          100.0%; Score 36; DB 2; Length 184;
Best local similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 EKSRTGD 7
DB 105 EKSRTGD 111

RESULT 2
A69829
ABC transporter (ATP-binding protein) homolog yhei - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C:Accession: A69829
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.: Bron, S.; Jrouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chai, A.; Ehrlich, S.D.; Emmerson, P.T.; Enslin, K.D.; Errington, J.; Fabret, C.; Ferrari, E. *Nature* 390, 249-256, 1997

A:Authors: Foulger, C.D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.C.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.; Kosterer, P.; Konigsleben, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Labber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Muehl, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelleid, Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seron, A.; Kuchel, M.; Tamakoshi, A.; Tanaka, T.; Terstap, P.; Tsoumou, K.; Tsutsumi, Y.; Uchiyama, T.; Winters, P.; Wippl, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: A69829

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-585 <KUN>

A:Cross-references: GB:29109; GB:AL009126; NID:92633260; PTDN:CBM12810.1; PID:92633306

A:Experimental source: strain 168

C:Genetics:

A:Gene: yhe1

C:Superfamily: Escherichia coli ABC transporter mdla; ATP-binding cassette homology E:354-558/Domain: ATP-binding cassette homology <ABC>

C:Keywords: ATP; nucleotide binding; P-loop

E:371-378/Region: nucleotide-binding motif A (P-loop)

```

Query Match          91.7%; Score 33; DB 2; Length 585;
Best Local Similarity 85.7%; Pred. No. 18;
Matches      6; Conservative    1; Mismatches      0; Indels      0; Gaps      0;

QY      1 EKSRTGD 7
        ||:|||||
Db       110 EKNRGTD 116

RESULT 3
A05028
IPQC protein homolog - common tobacco chloroplast
C:Species: chloroplast Nicotiana tabacum (common tobacco)
C:Idate: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-Apr-1995
C:Accession: A05028
R:Suglura, M.
submitted to the EMBL Data Library, August 1986
A:Reference number: A00149
A:Accession: A05028
A:Molecule type: DNA
A:Residues: 1-862 <SUG>
R:Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Zeraf, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohonoh, N.; Shimoto, J., 2043-2049, 1986
EMBO J. 5, 2043-2049, 1986
A>Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization, sites, features
A:Contents: annotation; gene organization, sites, features
C:Genetics:
A:Genome: chloroplast
A:start codon: TTC
C:keywords: chloroplast DNA-directed RNA polymerase beta'-2 chain
C:Keywords: chloroplast
```

Query Match	88.9%	Score 32	DB 2	Length 862
Best Local Similarity	85.7%	Pred. No. 47		
Matches	6	Conservative	1	Mismatches
			0	Indels
			0	Gaps
QY	1	EKSRSTD	7	
DB	609	EKSRSTD	615	

RESULT 4
S07137

DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - garden pea chloroplast (frag
C:Species: Chloroplast Pisum sativum (garden pea)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1999
C:Accession: S07137
R:Cozens, A.L.; Walker, J.E.
Biochem. J. 236, 453-460, 1986
A:Title: Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal subunit
A:Reference number: S07137; MUID:86323089; PMID:3530249
A:Accession: S07137
A:Molecule type: DNA
A:Residues: 1-1163 <COO>
A:Cross-references: EMBL:X03912; NID:G12137; PIDN:CAA27545.1; PID:9829325
C:Genetics:
A:Gene: rpoC2
A:Genome: chloroplast
A:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C:Keywords: chloroplast; nucleotidyltransferase; transcription

RESULT 5
A29959
DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - spinach chloroplast
C:Species: chloroplast Spinacia oleracea (Spinach)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Jun-1999
C:Accession: A29959
R:Hudson, G.S.; Holton, T.A.; Wittefeld, P.R.; Bottomley, W.
J. MOL. Biol. 200, 639-654, 1988
A:Title: Spinach chloroplast rpoB genes encode three subunits of the chloroplast RNA
A:Reference number: A29959; MUID:80310931; PMID:3045324
A:Accession: A29959
A:Molecule type: DNA
A:Residues: 1-1361 <HUD>
A:Cross-references: EMBL:M55297; NID:g295119; PIDN:AA04639.1; PID:g295122
C:Gene: rpoC-2
A:Genome: chloroplast
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match	88.9%	Score 32	DB 2	Length 1361
Best Local Similarity	85.7%	Pred. No. 77		
Matches	6	Conservative	1	Mismatches
			0	Indels
			0	Gaps
QY	1	EKSRITGD	7	
Db	1123	EKSRSGD	1129	

hypothetical protein SA0674 [imported] - *Staphylococcus aureus* (strain N315)
 H89843
 RESULT 6
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: H89843
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
 me, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
 C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, R.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: AB9758; MUID:21311952; PMID:11418146

A:Residues: 1-646 <KUR>
A:Cross-references: GB:BA000018; PID:q13700610; PIDN:BA041907.1; GSPDB:CN00149

A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0674
C:Superfamily: Bacillus subtilis probable anion-binding protein ylfle

Query Match 86.1%; Score 31; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
||| |||
DB 429 EKSMTGD 435

RESULT 7
E96615
hypothetical protein F16M22.3 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96615

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E96615

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1195 <STO>

A:Cross-references: GB:AE005173; NID:g11055842; PIDN:AAG28310.1; GSPDB:GN00141

C:Genetics:

A:Gene: F16M22.3

A:Map position: 1

Query Match 86.1%; Score 31; DB 2; Length 1195;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
||||| ||
DB 212 EKSRTGD 218

RESULT 8

AE3173
transcription regulator Atu5113 [imported] - Agrobacterium tumefaciens (strain C58, Dupc
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AE3173
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AE3173

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-92 <KUR>

A:Cross-references: GB:AE008687; PIDN:AL45803.1; PID:g17743541; GSPDB:GN00188

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu5113

A:Genome: plasmid

Query Match 83.3%; Score 30; DB 2; Length 92;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
||: |||||
DB 21 ERARTGD 27

RESULT 9

C97289
hypothetical protein CAC3165 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: C97289
R:Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;
J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C97289
A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-160 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81102.1; PID:g15026232; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3165

Query Match 83.3%; Score 30; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTG 6
||||| ||
DB 51 EKSRTG 56

RESULT 10

AH3650
glycosyl transferase (EC 2.4.1.-) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AH3650
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Iyano
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Le
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella meli
A:Reference number: AD3252; PMID:11756688

A:Accession: AH3650

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-396 <KUR>

A:Cross-references: GB:AE008918; PIDN:AL54371.1; PID:g17985355; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME11129

A:Map position: 11

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 83.3%; Score 30; DB 2; Length 396;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
|| |||||
DB 352 EKIRTD 358

RESULT 11

F04265
probable casein kinase (EC 2.7.1.-) - Arabidopsis thaliana
N:Alternate names: protein F20b18.210

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Sep-2001
 C:Accession: T04265
 R:Bayan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hehlsel, J.; Mewes, H.W.; Mayer, K.F.X
 Submitted to the Protein Sequence Database, March 1999
 A:Reference number: 215263
 A:Accession: T04265
 A:Molecule type: DNA
 A:Residues: 1-450 <BEV>
 A:Cross-references: EMBL:AL049483
 A:Experimental source: cultivar Columbia; BAC clone F20B18
 C:Genetics:
 A:Map position: 4
 A:Introns: 26/1; 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2; 238/3; 281/1; 308/3; 330
 A:Note: F20B18.210
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: phosphotransferase

Query Match 83.3%; Score 30; DB 2; Length 450;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 403 OKSRTGD 409

RESULT 12
 E72268
 A:Species: Thermotoga maritima (strain MSB8)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: E72268
 R:Nelson, K.E.; Claydon, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: E72268
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-463 <ARN>
 A:Cross-references: GB:AE001786; GB:AE000512; NID:94961873; PIDN:AAD36391.1; PID:9498187
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1317

Query Match 83.3%; Score 30; DB 2; Length 463;
 Best Local Similarity 85.7%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 308 EKSRTGD 314

RESULT 13
 S49641
 L-galactonolactone oxidase (EC 1.1.3.24) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: D-arabinono-1,4-lactone oxidase; protein YML086c
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 19-Apr-2002
 C:Accession: S49641; S61944
 R:Gentles, S.; Bowman, S.
 Submitted to the EMBL Data Library, November 1994
 A:Reference number: S49627
 A:Accession: S49641
 A:Molecule type: DNA
 A:Residues: 1-526 <GEN>
 A:Cross-references: EMBL:246660; NID:9575702; PID:9575717; MIPS:YML086C
 R:Hub, W.K.; Kim, S.T.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.
 Submitted to the EMBL Data Library, November 1995

A:Reference number: S61944
 A:Accession: S61944
 A:Molecule type: DNA
 A:Residues: 1-526 <HUB>
 A:Cross-references: EMBL:U40390; NID:91103916; PID:91103917
 A:Experimental source: strain ATCC 24858
 C:Genetics:
 A:Gene: SGD:AL01; ALO
 A:Cross-references: SGD:S0004551
 A:Map position: 13L
 C:Keywords: ascorbic acid biosynthesis; oxidoreductase; transmembrane protein
 F:172-188/Domain: transmembrane #status predicted <TM>

Query Match 83.3%; Score 30; DB 2; Length 526;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 293 EKSRTGD 299

RESULT 14
 H70441
 ribosomal protein L15 - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
 C:Accession: H70441
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: H70441
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-149 <AQF>
 A:Cross-references: GB:AE000749; NID:92983975; PIDN:AAC07532.1; PID:92983986; GB:AE00
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: rplO
 C:Superfamily: Escherichia coli ribosomal protein L15

Query Match 80.6%; Score 29; DB 2; Length 149;
 Best Local Similarity 71.4%; Pred. No. 35;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 39 OKSRTGD 45

RESULT 15
 E95307
 hypothetical protein Sma0669 [imported] - Sinorhizobium meliloti (strain 1021) magap1
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: E95307
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Kemp, C.; Abola, A.P.; Barloy-Hubier, F.; B
 ; Kalman, S.; Keeling, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
 ; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: E95307
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-316 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK65023.1; PID:914523453; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub
 pel, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0689
A:Genome: plasmid

Query Match		80.6%	Score 29;	DB 2;	length 316;
Best Local Similarity		71.4%	Pred. No. 79;		
Matches	5;	Conservative	2;	Mismatches	0;
Indels				Gaps	0;
OY	1	EKSRTGD	7		
	11	1111			
Db	221	EKARTGE	227		

Search completed: November 12, 2002, 17:01:02
Job time : 2.08155 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:49:26 : Search time 0.600858 Seconds

(without alignments)
483.139 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36

Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	184	TR17_HUMAN	Q02223 homo sapien
2	32	88.9	1163	RPOD_PEA	P12227 pismu sativ
3	32	88.9	1361	RPOD_SPIOL	P11704 spinacia ol
4	32	88.9	1376	RPOD_ARATH	P56164 arabidopsis
5	32	88.9	1384	RPOD_STNAL	O94755 sinapis alb
6	32	88.9	1388	RPOD_TOBAC	P38550 nicotiana t
7	30	83.3	526	ALO_YEAST	P54783 saccharomyc
8	30	83.3	1286	RPOD_GUITH	O78483 guillardia
9	29	80.6	149	RL15_AOUAE	O67561 aquifex aeo
10	29	80.6	1223	RPOD_MESVI	O9mns7 mesostigma
11	29	80.6	1351	RPOD_YEAST	P13433 saccharomyc
12	28	77.8	115	GLN1_METTH	O26758 methanobact
13	28	77.8	121	YCW1_YEAST	P25642 saccharomyc
14	28	77.8	128	Y598_MYCTU	Q10819 mycobacteri
15	28	77.8	288	T2D2_STRPN	P09357 streptococc
16	28	77.8	305	PIX1_XENLA	O94751 xenopus lae
17	28	77.8	321	CYE_GUITH	O78494 guillardia
18	28	77.8	346	HYPE_BRAJA	P31906 bradyrhizob
19	28	77.8	368	IDH2_KLULA	O94230 kluyveromyc
20	28	77.8	378	ALGL_PSEST	O911P2 pseudomonas
21	28	77.8	466	YDEU_ECOLI	P77288 escherichia
22	28	77.8	482	MANC_ECO57	O85472 escherichia
23	28	77.8	529	SP15_STRGR	P19471 streptomyce
24	28	77.8	589	MDLA_BUCAI	P57571 buchnera ap
25	28	77.8	608	AFAM_RAT	P36953 rattus norv
26	28	77.8	611	AFAM_MOUSE	O89020 mus musculu
27	28	77.8	626	Z143_HUMAN	P52747 homo sapien
28	28	77.8	727	COPA_ENTHR	P32113 enterococcu
29	28	77.8	728	UVRC_STRCO	O92512 streptomyce
30	28	77.8	1151	ITAI_HUMAN	P56199 homo sapien
31	28	77.8	1180	IF5A_PYRAE	P18614 rattus norv
32	27	75.0	138	IF5A_PYRAE	P56635 pyrobaculum
33	27	75.0	144	RL15_HAEIN	P44353 haemophilus

ALIGNMENTS

RESULT 1	TR17_HUMAN	STANDARD:	PRT: 184 AA.
ID	TR17_HUMAN		
AC	O02223:		
DT	01-JUL-1993 (Rel. 26, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).		
DE	TNFRSF17 OR BCMA OR BCM.		
GN	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.		
RC	Tissue-Peripheral blood leukocytes, and Lymph node;		
RC	MEDLINE=93010984; PubMed=1396583;		
RA	Laabl Y., Gras M.P., Carbonnel F., Brovet J.C., Berger R.,		
RA	Larsen C.J., Tsapis A.;		
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";		
RT	EMBO J. 11:3897-3904(1992).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=94218235; PubMed=8165126;		
RA	Laabl Y., Gras M.P., Brovet J.C., Berger R., Larsen C.J., Tsapis A.;		
RT	"The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";		
RT	Nucleic Acids Res. 22:1147-1154(1994).		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=99425270; PubMed=10493829;		
RA	Loftus B.J., Kim U.-J., Sneedon V.P., Kalush F., Brandon R.,		
RA	Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Croin L.,		
RA	Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,		
RA	Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;		
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";		
RT	Genomics 60:295-308(1999).		
RL	[4]		
RN	SEQUENCE FROM N.A., AND VARIANT THR-153.		
RP	MEDLINE=21419161; PubMed=11528522;		
RA	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;		
RT	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and Rheumatoid arthritis.";		
RT	Genes Immun. 2:276-279(2001).		
RL	[5]		
RN	FUNCTION.		
RP	MEDLINE=20363816; PubMed=10903733;		
RA	Hatzoglou A., Roussel J., Bourgade M.-F., Rogier E., Madry C.,		
RA	Inoue J., Devergne O., Tsapis A.;		
RT	"TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38		

34	27	75.0	184	1	Y5G7_CLOAB	P23672 clostridium
35	27	75.0	223	1	UGX2_YEAST	P32772 saccharomyc
36	27	75.0	227	1	CP22_COLGL	O00371 colletotric
37	27	75.0	236	1	YIHL_ECOLI	P23133 escherichia
38	27	75.0	240	1	YPBE_BACU3	P50731 bacillus su
39	27	75.0	287	1	SUHB_SYNY3	P74158 synechocyst
40	27	75.0	374	1	ALGL_AZOVI	O52195 azotobacter
41	27	75.0	394	1	GATR_MOUSE	P23336 mus musculu
42	27	75.0	410	1	YCFL_MESVI	O9mnsd mesostigma
43	27	75.0	429	1	SECY_AOUAE	O66491 aquifex aeo
44	27	75.0	437	1	SECY_BUCAI	P57571 buchnera ap
45	27	75.0	446	1	LAMB_ECO57	O8x5w7 escherichia

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE-20259066; PubMed-10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kinsvogel W., Clegg C.H.;
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RT Nature 404:995-999(2000).
 RN [7]
 RN FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RP MEDLINE-21170294; PubMed-10973284;
 RX Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Serosi I., Hsu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RT Nat. Immunol. 1:252-256(2000).
 RN [8]
 RN INTERACTION WITH TRAF5 AND TRAF6.
 RP MEDLINE-20381353; PubMed-10908663;
 RX Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF15/Bly5/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC EMBL; 214954; CAA78679.1; -;
 DR EMBL; 229575; CAA82691.1; -;
 DR EMBL; 229574; CAA82690.1; -;
 DR EMBL; 095742; AAB67251.1; -;
 DR EMBL; AB052772; BAB60895.1; -;
 DR PIR; S31208; S31208.
 DR PIR; S31209; S31209.
 DR Genew; HGNC:11913; TNFRSF17.
 DR MIM; 109545; -;
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 KM TRANSMEM 1 54
 FT DOMAIN 55 77
 FT TRANSMEM 55 77
 FT DOMAIN 1 54
 FT REPEAT 7 41
 FT SITE 3 4
 FT DISULFID 8 21
 FT DISULFID 24 37
 FT DISULFID 28 41
 FT VARIANT 153 153
 FT A -> T.
 FT /FTID=VAR_012224.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF1EE27670932 CRC64;

Query Match 100.0%; Score 36; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 EKSRTGD 7
 DB 105 EKSRTGD 111

 RESULT 2
 RPOD_PEA STANDARD; PRT; 1163 AA.
 AC P12227;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6) (Fragment).
 GN RPOC2.
 OS Pisum sativum (Garden pea).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86323089; PubMed-3530249;
 RA Cozens A.L., Walker J.E.;
 RT "Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal
 RT subunit S2 and the beta'-subunit of RNA polymerase.";
 RL Biochem. J. 236:453-460(1986).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
 CC {RNA}(n).
 CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 CC SUBUNITS: ALPHA, BETA', AND BETA".
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 CC -----
 CC EMBL; X03912; CAA27345.1; -;
 DR PIR; S07137; S07137.
 DR InterPro; IPR002879; RNA_pol_A2.
 DR Pfam; PF01854; RNA_pol_A2; 2.
 KW Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 1163 AA; 133598 MW; C92E7BEDA3FDB525 CRC64;

 Query Match 88.9%; Score 32; DB 1; Length 1163;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 EKSRTGD 7
 DB 924 EKSRTGD 930

 RESULT 3
 RPOD_SPIOI STANDARD; PRT; 1361 AA.
 AC P11704;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
 DE

```

GN RPOC2.
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Caryophyllales: Chenopodiaceae: Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88316931; PubMed=3045324;
RA Hudson G.S., Holton T.A., Whitefield P.R., Bottomley W.;
RT "Spinach chloroplast rpoBC genes encode three subunits of the
RT chloroplast RNA polymerase."
RL J. Mol. Biol. 200:639-654(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Geant d'hiver, and cv. Monato1;
RA MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Lineweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Mache R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization."
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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CC -----
DR EMBL: AJ400848; CAB88715.1; -.
DR PIR: A29959; A29959.
DR HSSP: Q9KWU6; 1HOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A.1.
DR Pfam: PF01854; RNA_pol_A2.2.
KW Transference; Transcription; DNA-directed RNA polymerase; Chloroplast.
SQ SEQUENCE 1361 AA; 154768 MW; 19F8C42BB1B17E8 CRC64;

Query Match      88.9%; Score 32; DB 1; Length 1361;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1123 EKSRTGD 1129

RESULT 4
RPOD_ARATH STANDARD; PRT; 1376 AA.
AC P56764;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneko T., Asanizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
RT thaliana."
RL DNA Res. 6:283-290(1999).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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CC -----
DR EMBL: AP000423; BAA84375.1; -.
DR HSSP: Q9KWU6; 1HOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A.1.
DR Pfam: PF01854; RNA_pol_A2.2.
KW Transference; Transcription; DNA-directed RNA polymerase; Chloroplast.
SQ SEQUENCE 1376 AA; 156365 MW; 7CB5820163E2B9D CRC64;

Query Match      88.9%; Score 32; DB 1; Length 1376;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1130 EKSRTGD 1136

RESULT 5
RPOD_SINAPL STANDARD; PRT; 1384 AA.
AC Q9THV5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Sinapis alba (white mustard) (Brassica hirta).
OC Chloroplast.
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 6-20.
RC STRAIN=cv. Albatros; TISSUE=cotyledon;
RX MEDLINE=20069369; PubMed=10601874;
RA Pfanschmidt T., Ogrzewalla K., Baginsky S., Stockmann A., Meyer H.E.,
RA Link G.;
RT "The multisubunit chloroplast RNA polymerase A from mustard (Sinapis
RT alba L.): integration of a prokaryotic core into a larger complex
RT with organelle-specific functions."
RL Eur. J. Biochem. 267:253-261(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR

```

CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".

CC -----

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CC -----

DR EMBL: AJ243754; CAB48415.2; -

DR HSSP: Q9KWU6; 1HOM.

DR InterPro: IPR000722; RNA_pol_A.

DR InterPro: IPR002879; RNA_pol_A2.

DR Pfam: PF00623; RNA_pol_A; 1.

DR Pfam: PF01854; RNA_pol_A2; 1.

KM Transference: Transcription: DNA-directed RNA polymerase: Chloroplast.

SO SEQUENCE 1388 AA; 157740 MW; 9A7BAD0205374A80 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1384;

Best Local Similarity 85.7%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7

DB 1138 EKSRSQD 1144

RESULT 6

PROD_TOBAC STANDARD; PRT; 1388 AA.

ID P38350;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE DNA-directed RNA polymerase beta* chain (EC 2.7.7.6).

GN RPOC2.

OS Nicotiana tabacum (Common tobacco).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4097;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Bright yellow 4;

RA Shinzaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,

RA Matsubayashi T., Zaita N., Chunmongse J., Obokata J.,

RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita M.,

RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,

RA Tondoh N., Shimada H., Sugita M.;

RT "The complete nucleotide sequence of the tobacco chloroplast genome:

RT its gene organization and expression.";

RL EMBO J. 5:2043-2049(1986).

RN [2]

RP REVISIONS.

RA MEDLINE=94003079; PubMed=8400137;

RA Oimstead R.G., Sweere J.A., Wolfe K.H.;

RT "Ninety extra nucleotide in ndhF gene of tobacco chloroplast DNA: a

RT summary of revisions to the 1986 genome sequence.";

RL Plant Mol. Biol. 22:1191-1193(1993).

CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

CC SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +

CC (RNA)(N).

CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR

CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".

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CC -----

DR EMBL: 200044; CAAT77410.1; ALT_SEQ.

DR HSSP: Q9KWU6; 1HOM.

DR InterPro: IPR000722; RNA_pol_A.

DR InterPro: IPR002879; RNA_pol_A2.

DR Pfam: PF00623; RNA_pol_A; 1.

DR Pfam: PF01854; RNA_pol_A2; 2.

KM Transference: Transcription: DNA-directed RNA polymerase: Chloroplast.

SO SEQUENCE 1388 AA; 156840 MW; 41FD7F238913186C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1388;

Best Local Similarity 85.7%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7

DB 1135 EKSRSQD 1141

RESULT 7

ALO_YEAST STANDARD; PRT; 526 AA.

ID ALO_YEAST

AC P54783; O42618;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE D-arabinono-1,4-lactone oxidase (EC 1.1.3.37) (ALO) (L-galactono-

DE gamma-lactone oxidase).

GN ALO1 OR YML086C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 86-105 AND 349-363.

RC STRAIN=ATCC 24858 / WH101;

RA MEDLINE=99140446; PubMed=10094636;

RA Huh W.-K., Lee B.-H., Kim S.-T., Kim Y.-R., Rhie G.-E., Baek Y.-W.,

RA Hwang C.-S., Lee J.-S., Kang S.-O.;

RT D-Erythraoscortic acid is an important antioxidant molecule in

RT Saccharomyces cerevisiae.";

RL Mol. Microbiol. 30:895-903(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Nishikimi M., Ohata Y., Ishikawa T.;

RT "Identification of the yeast genomic sequence encoding L-galactono-

RT gamma-lactone oxidase.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

RA Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: CAN OXIDIZE L-GULOONO-1,4-LACTONE AS WELL AS D-ARABINONO-

CC 1,4-LACTONE AND L-GALACTONO-1,4-LACTONE.

CC -1- CATALYTIC ACTIVITY: D-arabinono-1,4-lactone + O(2) = D-erythro-

CC ascorbate + H(2)O(2).

CC -1- COFACTOR: FAD.

CC -1- PATHWAY: D-erythraoscortic acid biosynthesis: final step.

CC -1- SUBCELLULAR LOCATION: Mitochondrial. Membrane-embedded.

CC -1- PTM: The N-terminus is blocked.

CC -1- SIMILARITY: Belongs to the oxygen-dependent FAD-linked

CC oxidoreductase family.

CC -----

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CC EMBL: UA0390; AAC98538.1; -.
DR EMBL: AB009401; BAA23804.1; -.
DR EMBL: Z46660; CAA86652.1; -.
DR SGD: S0004551; ALO1.
DR InterPro: IPR001575; Oxid_FAD_bind.
DR Pfam: PF01565; FAD_binding_4; 1.
DR PROSITE: PS00862; OX2_COVAL_FAD; 1.
KM Oxidoreductase: Flavoprotein; FAD: Mitochondrion: Membrane.
FT BINDING 56 56 FAD (COVALENT) (BY SIMILARITY).
FT CONFLICT 417 417 A -> P (IN REF. 2).
SQ SEQUENCE 526 AA; 59493 MW; 942177A74A738EC8 CRC64;

Query Match
Best Local Similarity 83.3%; Score 30; DB 1; Length 526;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 293 EKSRTGD 299

RESULT 8
ID RPOD_GUITH STANDARD; PRT: 1286 AA.
AC 078483;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Guillardia theta (Cryptomonas phi).
OC Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, Guillardia theta:
RT complete sequence and conserved synteny groups confirm its common
RT ancestry with red algae."
RL J. Mol. Evol. 48:236-244(1999).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC [RNA](N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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CC or send an email to license@lsb-sib.ch).
CC EMBL: AF041468; AAC35674.1; -.
DR HSSP: 09KMU6; 1HOM.
DR InterPro: IPR000722; RNA_POL_A.
DR InterPro: IPR002879; RNA_POL_A2.
DR Pfam: PF00663; RNA_POL_A; 1.
DR Pfam: PF01854; RNA_POL_A2; 2.
KM Transference; Transcription; DNA-directed RNA polymerase; Chloroplast.
SQ SEQUENCE 1286 AA; 145044 MW; BFFP46FEF5522C73 CRC64;

Query Match
Best Local Similarity 83.3%; Score 30; DB 1; Length 1286;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EKSRTGD 7
DB 972 EKSRTGD 978

RESULT 9
ID RL15_AQUAE STANDARD; PRT: 149 AA.
AC 067561;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L15.
GN RPL0 OR AQ_1642.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5.
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjaj M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@lsb-sib.ch).
CC EMBL: AE000749; AAC07532.1; -.
DR InterPro: IPR001196; Ribosomal_L15.
DR Pfam: PF00256; L15; 1.
DR Pfam: PF01305; Ribosomal_L15; 1.
DR TIGRfam: TIGR01071; rplD_bact; 1.
DR PROSITE: PS00475; RIBOSOMAL_L15; FALSE_NEG.
KM Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 149 AA; 16572 MW; 12BDD4E92D90357 CRC64;

Query Match
Best Local Similarity 80.6%; Score 29; DB 1; Length 149;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 39 QKSRTGD 45

RESULT 10
ID RPOD_MESVI STANDARD; PRT: 1223 AA.
AC 09MUS7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatoophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-NIES-296;
RX MEDLINE-20150907; PubMed-10668199;
RA Lemieux C., Otis C., Turmel M.;
RT "ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -----
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CC -----
DR EMBL: AF166114; AAF43824.1; -.
DR HSSP: Q9KMU6; 1HQH.
DR InterPro: IPR000722; RNA_POL_A.
DR InterPro: IPR002879; RNA_POL_A2.
DR Pfam: PF00623; RNA_POL_A; 1.
DR Pfam: PF01854; RNA_POL_A2; 2.
KW Transference: Transcription; DNA-directed RNA polymerase; Chloroplast.
SO SEQUENCE 1223 AA; 138048 MW; 4044E90805FC472A CRC64;

Query Match 80.6%; Score 29; DB 1; Length 1223;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRGCD 7
Db 987 ESKRTGD 993

RESULT 11
RPOK_YEAST STANDARD; PRT; 1351 AA.
ID RPOK_YEAST
AC P13433;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase, mitochondrial precursor (EC 2.7.7.6).
GN RPO41 OR YFL036W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-88002333; PubMed-3308116;
RA Masters B.S., Stohl L.L., Clayton D.A.;
RT "Yeast mitochondrial RNA polymerase is homologous to those encoded by
RT bacteriophages T3 and T7.";
RL Cell 51:89-99(1987).
RN [2]
RN SEQUENCE FROM N.A.
RX STRAIN-S288C / AB972;
RX MEDLINE-95400292; PubMed-7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasamura S.-I., Sasamura M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-266(1995).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

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CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE PHAGE AND MITOCHONDRIAL RNA POLYMERASES
CC FAMILY.
CC -----
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CC -----
DR EMBL: M17539; AAA35007.1; -.
DR EMBL: D50617; BAA09203.1; -.
DR PIR: A27336; A27336.
DR HSSP: P00573; 1AKO.
DR SGD: S0001858; RPO41.
DR InterPro: IPR002092; RNA_POL_phage.
DR Pfam: PF00940; RNA_POL_1.
DR PROSITE: PS00900; RNA_POL_PHAGE_1; 1.
DR PROSITE: PS00489; RNA_POL_PHAGE_2; 1.
KW Transference: DNA-directed RNA polymerase; Transcription;
KW Mitochondrion; Transist peptide.
FT TRANSIT 1 ? MITOCHONDRION.
FT CHAIN 1 ?
FT ACT_SITE 945 945 DNA-DIRECTED RNA POLYMERASE.
FT ACT_SITE 1014 1014 BY SIMILARITY.
FT ACT_SITE 1189 1189 BY SIMILARITY.
FT ACT_SITE 1485 1485 S -> G (IN REF. 2).
FT CONFLICT 900 901 KS -> NP (IN REF. 2).
SO SEQUENCE 1351 AA; 153080 MW; 505C8BCEB356F6 CRC64;

Query Match 80.6%; Score 29; DB 1; Length 1351;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRGCD 7
Db 899 ESKLTGD 905

RESULT 12
GLNL_METH STANDARD; PRT; 115 AA.
ID GLNL_METH
AC O26758;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitrogen regulatory protein P-II 1.
GN NTH662.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxId=187420;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-Delta H;
RX MEDLINE-98037514; PubMed-9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pochler B., Qiu D.,
RA Spadefora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- FUNCTION: COULD BE INVOLVED IN THE REGULATION OF NITROGEN
CC FIXATION.

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CC -1- SIMILARITY: BELONGS TO THE P(11) PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE000846; AAB85167.1; -
 CC HSSP: P05826; 2p11.
 CC InterPro: IPR002187; P11_glnb.
 CC Pfam: PF00543; P-11; 1.
 CC PRINTS: PR00340; P11GLNB.
 CC PRODOM: PD001194; P11_glnb; 1.
 CC PROSITE: PS00638; P11_Glnb_CTER; 1.
 CC Transcription regulation; Nitrogen fixation; Complete proteome.
 KW SEQUENCE 115 AA; 12904 MW; 4E77B0EA979BA53 CRC64;
 SO
 Query Match 77.8%; Score 28; DB 1; Length 115;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 EKSRTGD 7
 Db 82 ENARCTD 88
 RESULT 13
 YCWL YEAST STANDARD; PRT; 121 AA.
 ID YCWL YEAST
 AC P25642;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hypothetical 13.6 kDa protein in CPR4-SXK22 intergenic region.
 GN YCR071C OR YCR71C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 [1]
 RP SEQUENCE FROM N.A.
 RA Ballesta J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha M.,
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: SOME, TO S.POMBE SPAC3H8.03.
 CC -----
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 CC -----
 CC EMBL: X59720; CAA42269.1; -
 CC PIR: S19486; S19486.
 CC SGI: S0000667; IMG2.
 KW Hypothetical protein.
 SO SEQUENCE 121 AA; 13682 MW; F8E3304D6F38475A CRC64;
 Query Match 77.8%; Score 28; DB 1; Length 121;
 Best Local Similarity 71.4%; Pred. No. 21;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 EKSRTGD 7
 Db 69 ERSRTGN 75
 RESULT 14

YS98_MYCTU STANDARD; PRT; 128 AA.
 ID YS98_MYCTU
 AC 10819;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein RV2898C.
 GN RV2898C OR MT2966 OR MCV274.29C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteriales;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE UPF0102 FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z74024; CAA98371.1; -
 CC EMBL: AE007119; AAK47292.1; ALT_INT.
 DR TIGR: MT2966;
 DR TubercuList; RV2898C;
 DR InterPro: IPR003509; UPF0102.
 DR Pfam: PF02021; UPF0102; 1.
 DR TRIGPAMS; TIGR00252; TIGR00252; 1.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 128 AA; 14223 MW; BBEB1657FBDAF571 CRC64;
 Query Match 77.8%; Score 28; DB 1; Length 128;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 KSRTGD 7
 Db 61 KTRTGD-66
 RESULT 15
 T2D2_STRPN STANDARD; PRT; 288 AA.
 ID T2D2_STRPN
 AC P09357;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Type II restriction enzyme DpnII (EC 3.1.21.4) (Endonuclease DpnII)
GN (R.DpnII).
OS Streptococcus pneumoniae.
OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87002480; PubMed=3019562;
RA Lacks S.A., Mannarelli B.M., Springhorn S.S., Greenberg B.;
RT "Genetic basis of the complementary DpnI and DpnII restriction
RT systems of S. pneumoniae: an intercellular cassette mechanism.";
RL Cell 46:993-1000(1986).
RN [2]
RP SEQUENCE OF 1-11.
RX MEDLINE=88062686; PubMed=2824782;
RA de la Campa A.G., Purushottam K., Springhorn S.S., Lacks S.A.;
RT "Proteins encoded by the DpnII restriction gene cassette. Two
RT methylases and an endonuclease.";
RL J. Mol. Biol. 196:457-469(1987).
CC - FUNCTION: RECOGNIZES THE DOUBLE-STRANDED UNMETHYLATED SEQUENCE
CC GATC AND CLEAVES BEFORE G-1.
CC - CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC - SUBUNIT: HOMODIMER.
CC - SIMILARITY: TO R.MBOI AND R.LIAI.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M14339; AAA88582.1; -.
DR PIR: B24372; B24372.
DR REBASE: 777; DpnII.
KW Hydrolyase; Endonuclease; Nuclease; Restriction system.
SQ SEQUENCE 288 AA; 33585 MW; F7346EBA6940EB33 CRC64;

Query Match 77.88; Score 28; DB 1; Length 288;
Best Local Similarity 83.38; Pred. NO. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KSRTGD 7
1:|||||
DB 144 KNRTGD 149

Search completed: November 12, 2002, 16:58:59
Job time : 1.6086 secs

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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:16 : Search time 2.13305 Seconds
(without alignments)
676.183 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36

Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_unclassified:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	91.7	585	16	O07550
2	32	88.9	868	16	O8X140
3	32	88.9	1118	5	O9YD20
4	32	88.9	1186	5	O8T858
5	32	88.9	1332	8	O9H857
6	32	88.9	1386	8	O9H857
7	32	88.9	1389	10	O8S8Y1
8	31	86.1	1432	2	O9AG08
9	31	86.1	248	2	O82969
10	31	86.1	281	10	O8RMD7
11	31	86.1	646	16	O99Y04
12	31	86.1	1195	10	O9C730
13	31	86.1	1246	10	O9C609
14	30	83.3	79	17	O8ZTW7
15	30	83.3	92	16	O8UK19
16	30	83.3	160	16	O97EE8

17	30	83.3	351	10	O8RUB2	O8RUB2 oryza sativ
18	30	83.3	362	12	O91TF3	O91TF3 cat mosaic
19	30	83.3	362	10	O91TF2	O91TF2 cat mosaic
20	30	83.3	396	16	O81AX2	O81AX2 brucea me
21	30	83.3	439	5	O917X6	O917X6 drosophila
22	30	83.3	448	12	O91BP9	O91BP9 oat mosaic
23	30	83.3	450	10	O9SZ11	O9SZ11 arabidopsis
24	30	83.3	456	5	O46078	O46078 drosophila
25	30	83.3	463	16	O9X143	O9X143 thermotoga
26	30	83.3	499	2	O93678	O93678 pseudomonas
27	30	83.3	563	3	O8X050	O8X050 neurospora
28	30	83.3	743	11	O8R5B1	O8R5B1 mus musculu
29	30	83.3	1165	16	O99XX8	O99XX8 streptococc
30	30	83.3	2340	12	O8UZ27	O8UZ27 cat mosaic
31	29	80.6	140	2	O99072	O99072 desulfiloba
32	29	80.6	140	2	O9AEH3	O9AEH3 desulfiloba
33	29	80.6	156	2	O9ACF4	O9ACF4 uncultured
34	29	80.6	156	2	O9ACF3	O9ACF3 uncultured
35	29	80.6	156	2	O9ACF2	O9ACF2 uncultured
36	29	80.6	156	2	O9ACF1	O9ACF1 uncultured
37	29	80.6	189	2	O9AER0	O9AER0 denatobacte
38	29	80.6	198	2	O9AC94	O9AC94 desulfiloba
39	29	80.6	198	2	O9AC93	O9AC93 desulfiloba
40	29	80.6	199	2	O9AEC9	O9AEC9 desulfiloba
41	29	80.6	243	17	O8ZVW5	O8ZVW5 pyrobaculum
42	29	80.6	252	5	O9VK12	O9VK12 drosophila
43	29	80.6	310	2	O93956	O93956 desulfiloba
44	29	80.6	316	2	O93955	O93955 desulfiloba
45	29	80.6	316	2	O93953	O93953 desulfiloba

ALIGNMENTS

RESULT 1

ID	O07550	PRELIMINARY:	PRT:	585 AA.
AC	O07550:			
DT	01-JUL-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Hypothetical protein yhe1.			
GN	yhe1.			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;			
OC	Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168:			
RL	Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;			
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=98044033; PubMed=9384377;			
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,			
RA	Azevedo V., Bortner M.G., Bessieres P., Bolotin A., Borchert S.,			
RA	Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,			
RA	Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,			
RA	Choi S.K., Codan J.J., Connerton I.F., Cummings N.J., Daniel R.A.,			
RA	Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,			
RA	Ertlan K.D., Errington J., Fabel C., Ferrari E., Foulger D.,			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,			
RA	Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,			
RA	Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,			
RA	Hilbert B., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,			
RA	Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,			
RA	Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,			
RA	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,			
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,			
RA	Medina N., Mellado R.P., Mizuno M., Moestil D., Nakai S., Noback M.,			
RA	Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,			

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RA Parro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Priesean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche A., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowaka A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,
RA Vlati A., Wambutt R., Wedler E., Wedler R., Welzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168:
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
DR EMBL: Y14080; CA74450.1; -.
DR EMBL: 299109; CAB12810.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00664; ABC_membrane.1.
DR Pfam: PF00005; ABC_tran.1.
DR ProDom: PD000006; ABC_transportr.1.
DR SMART: SM00382; AAA.1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding: Hypothetical protein; Transport; Complete proteome.
KW SEQUENCE 585 AA; 6511 MW; AB82FA64338F6161 CRC64;
SQ
Query Match 91.7%; Score 33; DB 16; Length 585;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 110 EKNRTCD 116
RESULT 2
OEXL40 PRELIMINARY; PRT; 868 AA.
AC O8XL40:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Probable calcium-transporting ATPase.
GN CPE1202.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-13 / TYPE A;
RA Pubmed-11792842;
RA Shimaizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AF003189; BAB80908.1; -.
DR InterPro: IPR00157; ATPase_E1-E2.
DR InterPro: IPR004014; Cation_ATPase.
DR InterPro: IPR000661; H/K_Na/K_ATPase.
DR InterPro: IPR001454; Hlg_nase/hydriase.
DR InterPro: IPR001245; Ty_r_kinase.
DR Pfam: PF00689; Cation_ATPase_C; 1.

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DR Pfam: PF00690; Cation_ATPase_N; 1.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00702; Hydrolase; 1.
DR PRINTS: PR00119; CATAPPASE.
DR PROSITE: PS00154; ATPASE_E1-E2; UNKNOWN.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN.1.
KW Complete proteome.
SQ SEQUENCE 868 AA; 95746 MW; 1381A132261AC237 CRC64;
Query Match 88.9%; Score 32; DB 16; Length 868;
Best Local Similarity 85.7%; Pred. No. 116+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 376 EKSRTGD 382
RESULT 3
O9VD20 PRELIMINARY; PRT; 1118 AA.
AC O9VD20:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE CG18427 OR CG12757.
GN CG18427 OR CG12757.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY:
RA MEDLINE-20196006; Pubmed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foster C., Gongalian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gang F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei J., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paule J.M.,
RA Palazzolo M., Peltum G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Ventle E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

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RL Science 287:2185-2195(2000).
CC -1- CATALYTIC ACTIVITY: SN-GLYCEROL 3-PHOSPHATE + NAD(+) - GLYCERONE
CC PHOSPHATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE NAD-DEPENDENT GLYCEROL 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL: AE003738; AAF55983.1; -.
DR FLYbase: FBgn0038955; CG18427.
DR InterPro: IPR001652; NAD_GLY3P_dh.
DR Pfam: PF01210; NAD_GLY3P_dh: 1.
DR PRINTS: PR00077; GPDHRCNASE.
KW NAD: Oxidoreductase.
SQ SEQUENCE 1118 AA; 125080 MW; 356E3746E9559ED6 CRC64;

Query Match 88.9%; Score 32; DB 5; Length 1118;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 986 EKDRGTD 992

RESULT 4
Q8T8S8 PRELIMINARY; PRT; 1186 AA.
AC Q8T8S8;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE AT30755p.
DE AT30755p.
GN CG18427.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorselt V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Murgall C.J., Nunoo J., Paclet J., Paragas V., Park S.,
RA Patel S., Phouenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RD EMBL: At073291; AAL68158.1; -.
SQ SEQUENCE 1186 AA; 133529 MW; EC2606999C5EF36A CRC64;

Query Match 88.9%; Score 32; DB 5; Length 1186;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1054 EKDRGTD 1060

RESULT 5
Q9BBS7 PRELIMINARY; PRT; 1332 AA.
AC Q9BBS7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE RNA polymerase beta' subunit-2.
GN RPOC2.
OS Lotus japonicus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=ACCESSION MG-20;
RA Kato T.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ACCESSION MG-20;
RX MEDLINE-21082929; PubMed-11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus";
RL DNA Res. 7:323-330(2000).
DR EMBL: AP002983; BAB33196.1; -.
DR HSSP: Q9KMU6; 1HOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A: 1.
DR Pfam: PF01854; RNA_pol_A2; 2.
KW Chloroplast.
SQ SEQUENCE 1332 AA; 151852 MW; BDA32FF920B2B8C1 CRC64;

Query Match 88.9%; Score 32; DB 8; Length 1332;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1112 EKSRSGD 1118

RESULT 6
Q9MTM3 PRELIMINARY; PRT; 1386 AA.
AC Q9MTM3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE RNA polymerase beta' subunit.
GN RPOC2.
OS Oenothera hookeri (Hooker's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=85636;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20309318; PubMed-10852478;
RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Mäler R.M.,
RA Chiu W.L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT Euphonia plastomes.";
RL Mol. Gen. Genet. 263:581-585(2000).
RL EMBL: AJ271079; CAB67153.1; -.
DR HSSP: Q9KMU6; 1HOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A: 1.
DR Pfam: PF01854; RNA_pol_A2; 2.
KW Chloroplast.
SQ SEQUENCE 1386 AA; 157202 MW; 720B5DAC30AD5ED0 CRC64;

Query Match 88.9%; Score 32; DB 8; Length 1386;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1134 EKSRSGD 1140

RESULT 7

Q88Y1 ID Q88Y1 PRELIMINARY; PRT; 1389 AA.
 AC Q88Y1;
 DT 01-JUN-2002 (TReMBrel. 21, Created)
 DT 01-JUN-2002 (TReMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBrel. 21, Last annotation update)
 DE RNA polymerase beta II subunit.
 GN RPOC2.
 OS Atropa belladonna (Belladonna) (Deadly nightshade).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
 OX NCBI_TaxID=33113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ABSP(KAN);
 RA Schmitz-Glinne Weber C., Regel R., Gla Du T., Hupfer H., Herrmann R.G.,
 RA Meier R.M.;
 RT "The nucleotide sequence of the plastid chromosome of Atropa
 RT belladonna (deadly nightshade) and its comparison with that of
 RT Nicotiana tabacum with emphasis on sequence elements relevant for
 RT microevolution."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ15582; CAC88034.1; -;
 SO SEQUENCE 1389 AA; 156857 MW; 987B9E096CB4B1D5 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 1389;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRGCD 7
 Db 1136 EKSRGCD 1142

RESULT 8
 Q9AG08 ID Q9AG08 PRELIMINARY; PRT; 132 AA.
 AC Q9AG08;
 DT 01-JUN-2001 (TReMBrel. 17, Created)
 DT 01-JUN-2001 (TReMBrel. 17, Last sequence update)
 DT 01-JUN-2002 (TReMBrel. 21, Last annotation update)
 DE Ribosomal binding factor A.
 GN RBP A.
 OS Wolbachia sp. wrl.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Wolbachieae; Wolbachia.
 OX NCBI_TaxID=66084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WRI;
 RA Sun L.V., O'Neill S.L.;
 RT "Genomic organization of the upstream region of the Wolbachia dnaA
 RT gene."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF348330; AK31156.1;
 DR InterPro: IPR000238; Rib_bind_facta.
 DR Pfam: PF02033; RBP A. 1;
 SO SEQUENCE 132 AA; 15102 MW; 24BCF395F43CADF CRC64;

Query Match 86.1%; Score 31; DB 2; Length 132;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRGCD 7
 Db 66 EKSRGCD 72

RESULT 9
 ID Q82969 PRELIMINARY; PRT; 248 AA.
 AC Q82969;

DT 01-NOV-1998 (TReMBrel. 08, Created)
 DT 01-NOV-1998 (TReMBrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBrel. 19, Last annotation update)
 DE A2-5a orf1 (Fragment).
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1409;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261044; PubMed=10803899;
 RA Ohdan K., Kuriki T., Takata H., Okada S.;
 RT "Cloning of the cyclodextrin glucanotransferase gene from alkalophilic
 RT Bacillus sp. A2-5a and analysis of the raw starch-binding domain."
 RL Appl. Microbiol. Biotechnol. 53:430-434(2000).
 DR EMBL: AB015670; BAA31529.1; -;
 FT NON_TER 1
 SO SEQUENCE 248 AA; 27286 MW; DB9322A115442722 CRC64;

Query Match 86.1%; Score 31; DB 2; Length 248;
 Best Local Similarity 85.7%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRGCD 7
 Db 148 EKSRGCD 154

RESULT 10
 Q8RWD7 ID Q8RWD7 PRELIMINARY; PRT; 281 AA.
 AC Q8RWD7;
 DT 01-JUN-2002 (TReMBrel. 21, Created)
 DT 01-JUN-2002 (TReMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBrel. 21, Last annotation update)
 DE Hypothetical 31.6 kDa protein.
 GN AT1G38210.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carlini P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kanliya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY093160; AAM13159.1; -;
 KW Hypothetical protein.
 SO SEQUENCE 281 AA; 31560 MW; 27EA3BE74F89528 CRC64;

Query Match 86.1%; Score 31; DB 10; Length 281;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRGCD 7
 Db 212 EKSRGCD 218

RESULT 11
 Q99VQ4 ID Q99VQ4 PRELIMINARY; PRT; 646 AA.
 AC Q99VQ4;
 DT 01-JUN-2001 (TReMBrel. 17, Created)
 DT 01-JUN-2001 (TReMBrel. 17, Last sequence update)
 DT 01-MAR-2002 (TReMBrel. 20, Last annotation update)
 DE Hypothetical protein SAV0719.
 GN SAV0719 OR SA0674.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria: Firmicutes, Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 NC NCBITaxID=158878, 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
 RX MEDLINE=2111952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh Y., Ito T.,
 Kanemori M., Matsumaru H., Maruyama A., Hoshino A.,
 Mizutani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hiramatsu H., Kohara S., Goto S., Yabuzaki J.,
 Kanohisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003360; BAB56881.1; -;
 DR EMBL: AP003131; BAB41907.1; -;
 DR InterPro: IPR000917; Sulfatase.
 DR Pfam: PF00884; Sulfatase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 646 AA; 74400 MW; 788FE36B4528B0 CRC64;

Query Match
 Best Local Similarity 86.1%; Score 31; DB 16; Length 646;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 429 EKSRTGD 435

RESULT 12
 G9C730
 ID 09C730 PRELIMINARY; PRT: 1195 AA.
 AC 09C730;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DE Hypothetical 135.5 kDa protein.
 GN F16M22.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NC NCBITaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzer S.L., Tambunga G., Toriumi M.J., Town C.D.,
 Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RT thaliana.";
 RL Nature 408:816-820(2000).
 DR EMBL: AC079131; AAG50760.1; -;
 DR InterPro: IPR001064; Crystallin.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1246 AA; 140995 MW; BE23EE9DC47F3F8 CMC64;

Query Match
 Best Local Similarity 86.1%; Score 31; DB 10; Length 1246;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 212 EKSRTGD 218

RESULT 13
 G9C609
 ID 09C609 PRELIMINARY; PRT: 1246 AA.
 AC 09C609;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Hypothetical 141.0 kDa protein.
 GN T18124.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NC NCBITaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RT thaliana.";
 RL Nature 408:816-820(2000).
 DR EMBL: AC079131; AAG50760.1; -;
 DR InterPro: IPR001064; Crystallin.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1246 AA; 140995 MW; BE23EE9DC47F3F8 CMC64;

Query Match
 Best Local Similarity 86.1%; Score 31; DB 10; Length 1246;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 Db 212 EKSRTGD 218

RESULT 14
 G82TW7
 ID 082TW7 PRELIMINARY; PRT: 79 AA.
 AC 082TW7;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

Search completed: November 12, 2002, 17:00:20
 Job time : 4.13305 secs

DE Hypothetical protein PAE3058.
 GN PAE3058.
 OS Pyrobaculum aerophilum.
 OC Archaea: Crenarchaeota: Thermoprotei: Thermoproteales;
 OC Thermoproteaceae: Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Flitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 DR EMBL: AE009908; AAL64642.1; -.
 DR InterPro: IPR002792; TRAM.
 DR Pfam: PF01938; TRAM; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 79 AA; 8695 MW; B36D5871B6C30143 CRC64;

Query Match 83.3%; Score 30; DB 17; Length 79;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRGCD 7
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 DB 34 EKSRGCD 40

RESULT 15
 Q8UK19

ID Q8UK19 PRELIMINARY; PRT; 92 AA.
 AC Q8UK19;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Transcriptional regulator.
 GN ATU5113.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Plasmid AT.
 OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group;
 OC Rhizobiaceae: Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutyavin T., Levy R., Li M.-J., McElleland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323(2001).
 DR EMBL: AE008936; AAL45803.1; -.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 92 AA; 10349 MW; 51B37E9FD71DF6D2 CRC64;

Query Match 83.3%; Score 30; DB 16; Length 92;
 Best Local Similarity 71.4%; Pred. No. 25;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRGCD 7
 |||||
 DB 21 EKSRGCD 27

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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:48:46 : Search time 16.0429 Seconds
(without alignments)
348.847 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45

Perfect score: 239
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Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	100.0	51	23	AAE15485 Human B-cell matur
2	239	100.0	181	23	AAE15484 Human B-cell matur
3	239	100.0	184	21	AAB08843 Amino acid sequenc
4	239	100.0	184	21	AAE94001 A human BCMA prote
5	239	100.0	184	22	AAE09241 Human BCMA protein
6	239	100.0	184	22	AAE05056 Human B cell matur
7	239	100.0	184	22	AAB60698 Human BAF receptor
8	239	100.0	184	22	AAV71979 Human B cell matur
9	239	100.0	184	23	AAB81487 Human BCMA recepto
10	239	100.0	283	23	AAE15488 Human BCMA-immunog

11	239	100.0	302	22	AAE00507 Human BCMA-immunog
12	239	100.0	302	22	AAB60699 Mouse IgG signal/h
13	219	91.6	58	23	AAE15501 Human B-cell matur
14	201	84.1	34	23	AAE15486 Human B-cell matur
15	181	75.7	157	22	AAB60700 Human BAF recepto
16	156	65.3	185	21	AAB08844 Amino acid sequenc
17	156	65.3	185	22	AAE15488 Murine B cell matur
18	156	65.3	185	23	AAE15490 Mouse B cell matur
19	156	65.3	281	23	AAE15489 Mouse BCMA-human
20	95.5	40.0	117	23	AAE15491 Human-murine B cel
21	90.5	37.9	24	23	AAE15492 Human-murine BCMA
22	71.5	29.9	249	21	AAE15493 A murine zlf4, a
23	67.5	28.2	37	23	AAU10951 Human AGP-3 recept
24	67.5	28.2	59	23	AAE15500 Human AGP-3 recept
25	67.5	28.2	166	19	AAE15785 Human lymphocyte s
26	67.5	28.2	166	23	AAE15494 Human TACI extrace
27	67.5	28.2	265	22	AAE09244 Human TACI splice
28	67.5	28.2	291	23	AAU10949 Human AGP-3 recept
29	67.5	28.2	293	19	AAE15783 Human lymphocyte s
30	67.5	28.2	293	21	AAE15490 Human neutrokin-a
31	67.5	28.2	293	21	AAE15490 A transmembrane ac
32	67.5	28.2	293	22	AAE09240 Human TACI protein
33	67.5	28.2	293	22	AAE15493 Human tumour necro
34	67.5	28.2	293	23	AAU10949 Human TACI-IgG Fc
35	67.5	28.2	293	23	AAB81488 Human TACI recepto
36	67.5	28.2	293	23	AAO14130 Human transmembran
37	67.5	28.2	293	23	AAU75408 Tumour necrosis fa
38	67.5	28.2	293	23	AAE15493 Human transmembran
39	67.5	28.2	293	23	AAU09900 Human AGP-3 relate
40	67.5	28.2	312	23	AAO14135 Protein of N-termi
41	67.5	28.2	334	23	AAO14133 Protein of hTACI (
42	67.5	28.2	365	23	AAO14132 Human TACI-immunog
43	67.5	28.2	397	23	AAE15498 Protein of a compl
44	67.5	28.2	404	23	AAO14136 Human TACI cystein
45	66.5	27.8	33	23	AAE15495

ALIGNMENTS

RESULT 1	AAE15485	AAE15485 standard; peptide: 51 AA.
ID	AAE15485	
AC	AAE15485:	
XX		
DT	12-MAR-2002 (first entry)	
XX		
DE		
XX		
XX	Human B-cell maturation (BCMA) protein extracellular domain.	
XX		
XX	Human: transmembrane activator and intracellular CAML interactor; TACI;	
XX	cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;	
XX	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;	
XX	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;	
XX	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;	
XX	Crown's disease; scleroderma; autoimmune disease; multiple sclerosis;	
XX	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;	
XX	rheumatoid arthritis; atherosclerosis.	
OS	Homo sapiens.	
XX		
XX	WO200187979-A2.	
XX		
XX	22-NOV-2001.	
XX		
XX	14-MAY-2001; 2001WO-US15567.	
XX		
XX	12-MAY-2000; 2000US-204039P.	
XX	27-JUN-2000; 2000US-214591P.	
XX	14-MAY-2001; 2001US-0214591.	
XX		
XX	(AMCE-) AMGEN INC.	

PI The11 LE, Yu G;
XX WPI: 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX
PS Claim 1: Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein extracellular domain.
XX
XX Sequence 51 AA:
SO
Query Match 100.0%; Score 239; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 4,4e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAGGCSQNEYFDSLHACIPQLRCSNPPPLTCQRYCNASV 42
DB 1 MAGGCSQNEYFDSLHACIPQLRCSNPPPLTCQRYCNASV 42
RESULT 2
AAE15484
ID AAE15484 standard: Protein; 181 AA.
XX
AC AAE15484;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein.
XX
XX Human: transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 5..38
FT /note= "Cysteine-rich consensus region: This is region
FT is specifically claimed as SEQ ID NO: 7 in claim 1 of
FT the specification"
FT Domain 52..72
FT /label= "Transmembrane_domain"
XX
XX WO200187979-A2.
XX

PD 22-NOV-2001.
XX
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX The11 LE, Yu G;
XX WPI: 2002-066686/09.
XX
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX
XX Disclosure: Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein.
XX
XX Sequence 181 AA:
SO
Query Match 100.0%; Score 239; DB 23; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAGGCSQNEYFDSLHACIPQLRCSNPPPLTCQRYCNASV 42
DB 1 MAGGCSQNEYFDSLHACIPQLRCSNPPPLTCQRYCNASV 42
RESULT 3
AAB08843
ID AAB08843 standard: peptide; 184 AA.
XX
XX AAB08843;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of human.
XX
XX BCMA: necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 57..77
FT /note= "putative transmembrane domain"
XX
XX WO200050633-A1.
XX

XX 31-AUG-2000.
PD 24-FEB-2000; 2000MO-US04925.
XX PF 24-FEB-1999; 9905-0121485.
XX PR (GEHO) GEN HOSPITAL CORP.
XX PA Seed B, Ting A;
XX PI WPI: 2000-558405/51.
XX DR Identifying a modulator of gene expression for drug designing, by
XX PT contacting a compound library with a cell expressing an anti-cell death
XX PT gene and reporter gene, and determining alteration in reporter gene
XX PT expression -
XX PS Claim 32; Fig 7A; 53pp; English.
XX PS The present sequence represents a BCMA (not defined) polypeptide. BCMA
CC is a necrosis factor (NF)-KB activator. The method of the invention is
CC used to identify compounds which modulate BCMA activity (and thus NF-KB
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to
CC the promoter, and then determining whether the expression of the
CC reporter gene is altered as a result of contact with library. The method
CC is useful for identifying polypeptides which increase or decrease gene
CC expression from a promoter. The BCMA polypeptide or nucleic acid are
CC useful for preparing a pharmaceutical composition for treating cancer,
CC apoptosis, viral infections, inflammatory response, such as rheumatoid
CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
CC identifying compounds that modulate NF-KB expression and thus for drug
CC designing.
SQ Sequence 184 AA:
Query Match 100.0%; Score 239; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGCCSQNEFYFDSLHACIFCQRLRCSSNTPPLTCQRCNNAV 42
DB 4 MAGCCSQNEFYFDSLHACIFCQRLRCSSNTPPLTCQRCNNAV 45
RESULT 4
ID AAY94001 standard; Protein; 184 AA.
XX AC AAY94001;
XX DT 20-OCT-2000 (first entry)
XX DE A human BCMA protein, a B cell protein related to TACI.
XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX KW renal neoplasms; multiple myeloma; lymphoma; light chain neuropathy;
XX KW immune response; immunosuppression; graft rejection; joint pain;
XX KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX OS Homo sapiens.
XX PN WO200040716-A2.
XX PN

XX 13-JUL-2000.
PD 07-JAN-2000; 2000MO-US00396.
XX PF 07-JAN-1999; 9905-0226533.
XX PR (ZYMO) ZYMOGENETICS INC.
XX PA Gross JA, Xu W, Madden K, Yee DP;
XX PI WPI: 2000-452538/39.
XX DR N-PSDB: AAA58559.
XX DR Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
XX PT renal disease, graft versus host disease, and inflammation, comprises
XX PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX PS Disclosure; Page 152; 175pp; English.
XX PS The present sequence represents a human BCMA protein, a B cell protein
CC related to transmembrane activator and CAML-interactor (TACI) receptor.
CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
CC protein) receptor contain a cysteine rich domain, and are used for
CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC with activated or resting B lymphocytes, effector T-cells, or with
CC antibody production. The antibody production is associated with an
CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC asthma, bronchitis, emphysema, end stage renal failure,
CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC amyloidosis, moderating immune response, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli.
SQ Sequence 184 AA:
Query Match 100.0%; Score 239; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGCCSQNEFYFDSLHACIFCQRLRCSSNTPPLTCQRCNNAV 42
DB 4 MAGCCSQNEFYFDSLHACIFCQRLRCSSNTPPLTCQRCNNAV 45
RESULT 5
ID AAE09241 standard; Protein; 184 AA.
XX AC AAE09241;
XX DT 19-NOV-2001 (first entry)
XX DE Human BCMA protein.
XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
XX KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX KW psoriasis.
XX OS Homo sapiens.
XX PN WO200160397-A1.
XX PN 23-AUG-2001.
XX PD

```
XX 28-NOV-2000; 2000MO-US32378.
XX
XX 16-FEB-2000; 2000US-0182938.
PR
XX 22-AUG-2000; 2000US-0226986.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pittl RM;
PI Yan M;
XX
XX WPI: 2001-541628/60.
DR N-PSDB; AAD05902.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
XX Example 2; Fig 2; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. Rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC BCMA protein.
XX
SQ Sequence 184 AA;
XX
XX
XX Query Match 100.0%; Score 239; DB 22; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-21;
XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MAGCCSONEYFDSLHACIPCOLRCSSNTPTLCORCNASV 42
DB 4 MAGCCSONEYFDSLHACIPCOLRCSSNTPTLCORCNASV 45
XX
XX
XX RESULT 6
XX ID AAE00506 standard; protein; 184 AA.
XX AC AAE00506;
XX
XX 31-JUL-2001 (first entry)
XX
XX Human B cell maturation protein (BCMA).
XX
XX Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF;
XX tumour necrosis factor; BCMA; B cell maturation protein.
XX
XX Homo sapiens.
XX
XX MO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000MO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX
XX 11-FEB-2000; 2000US-0181807.
XX
PR
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PR 30-JUN-2000; 2000US-0215688.
XX
XX (BIOJ ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX
XX WPI: 2001-266242/27.
DR N-PSDB; AAD03844.
XX
XX Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor
PT (APRIL-R) antagonist -
XX
XX Claim 3; Fig 3A; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or
CC carcinoma. The method involves administering a composition comprising
CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC human immunodeficiency virus (HIV), and for treating, suppressing or
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is human APRIL-R also referred as BCMA or
CC BCM protein.
XX
XX
XX Sequence 184 AA;
XX
XX
XX Query Match 100.0%; Score 239; DB 22; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-21;
XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MAGCCSONEYFDSLHACIPCOLRCSSNTPTLCORCNASV 42
DB 4 MAGCCSONEYFDSLHACIPCOLRCSSNTPTLCORCNASV 45
XX
XX
XX RESULT 7
XX ID AAB60698 standard; protein; 184 AA.
XX AC AAB60698;
XX
XX 22-MAY-2001 (first entry)
XX
XX Human BAFF receptor (BAFF-R).
XX
XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor; BCMA;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX renal disorder; immunosuppressive disorder; HIV infection;
XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX lymphoma; gene therapy; cancer; tumour.
XX
XX Homo sapiens.
XX
XX MO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX
```

PF 16-AUG-2000; 2000MO-US22507.
 XX
 XX 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,
 PI Thompson J;
 DR MPI: 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAF-R-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAF-R
 PT antibody homolog
 XX
 PS Claim 20: Fig 1; 59pp; English.
 XX
 CC The invention relates to the use of a BAF-R receptor (BAF-R, also known
 CC as BCMA) protein, or a BAF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAF-R, fusion proteins containing it, and BAF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAF-R
 CC proteins or BAF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAF-R and BAF-R, thereby inhibiting inflammation. Since BAF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAF-R.
 XX
 SO Sequence 184 AA;
 Query Match 100.0%; Score 239; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.7e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGCSONEYFDSLHACIPQLRCSSNPPLTCQRYCNASV 42
 Db 4 MAGCSONEYFDSLHACIPQLRCSSNPPLTCQRYCNASV 45
 RESULT 8
 AAY71979
 ID AAY71979 standard; Protein; 184 AA.
 XX
 XX AAY71979;
 DT 28-MAR-2001 (first entry)
 XX
 DE Human B cell maturation factor (BCMA) protein.
 XX
 KW Human: Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;

KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 OS
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..62
 XX /label= Extracellular_domain
 XX
 PN MO200068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000MO-US12266.
 XX
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Shu HS;
 DR MPI: 2001-016094/02.
 DR N-PSDB; AAD02125.
 XX
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 PS Claim 37: Page 104-105; 112pp; English.
 XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16. In human tissues, BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.
 XX
 SO Sequence 184 AA;
 Query Match 100.0%; Score 239; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.7e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGCSONEYFDSLHACIPQLRCSSNPPLTCQRYCNASV 42
 Db 4 MAGCSONEYFDSLHACIPQLRCSSNPPLTCQRYCNASV 45
 RESULT 9
 ABB81487
 ID ABB81487 standard; Protein; 184 AA.
 XX
 XX ABB81487;
 AC
 AC ABB81487;
 XX
 DT 02-SEP-2002 (first entry)
 XX

DE Human BCMA receptor related protein SEQ ID NO:7.

XX Human; Znf112; tumour necrosis factor receptor; cytosolic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

PN WO200238766-A2.

XX 16-MAY-2002.

XX 05-NOV-2001; 2001WO-0547018.

XX 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.

PR 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

PI Gross JA, Xu W, Henne RM, Grant FJ;

XX WPI; 2002-508212/54.

PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT zcnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma

PS Disclosure: Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated znf112 (1). (1) has cytosolic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (1) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds znf112
 CC (e.g. zymf4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (1) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (1) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.

XX Sequence 184 AA;

SO Query Match 100.0%; Score 239; DB 23; Length 184;

Best local Similarity 100.0%; Pred. No. 1.7e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGGCSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYCNASV 42

DB 4 MAGGCSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYCNASV 45

RESULT 10
 AAEL5488
 ID AAEL5488 standard; Protein; 283 AA.

XX AAEL5488;

XX 12-MAR-2002 (first entry)

DE Human BCMA-immunoglobulin Fc region fusion protein.

XX Human: transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.

XX Homo sapiens.

PN WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-0515567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand

PS Disclosure: Fig 10B; 94pp; English.

XX The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein.

XX Sequence 283 AA;

SO Query Match 100.0%; Score 239; DB 23; Length 283;

Best local Similarity 100.0%; Pred. No. 2.6e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGGCSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYCNASV 42

DB 1 MAGGCSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYCNASV 42

CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAF-R, fusion proteins containing it, and BAF-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAF-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAF-R
CC proteins or BAF-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinoma, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents the BAF-R fusion protein BAF-R-Fc,
CC comprising a mouse IgG-kappa signal sequence, residues 1-153
CC of human BAF-R and a human IgG Fc sequence.
CC
CC
SQ Sequence 302 AA;

Query Match 100.0%; Score 239; DB 22; Length 302;
Best Local Similarity 100.0%; Pred. No. 2,8e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGCSONEYFDSLHCIPQLRCSSNTPPLTCORCNASY 42
Db 27 MAGCSONEYFDSLHCIPQLRCSSNTPPLTCORCNASY 68
|||||

RESULT 13
ID AAE15501 standard; peptide: 58 AA.
AAE15501:
AC AAE15501:
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX

DE Human B cell maturation protein cysteine rich extracellular region.
XX

KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX

OS Homo sapiens.
XX

PN WO200187979-A2.
XX

PD 22-NOV-2001.
XX

PE 14-MAY-2001; 2001WO-US15567.
XX

PF 12-MAY-2000; 2000US-204039P.
XX

PR 27-JUN-2000; 2000US-214591P.
XX

PA 14-MAY-2001; 2001US-0214591.
XX

PI (AMGE-) AMGEN INC.
XX

PI Theill LE, Yu G;
XX

WPI: 2002-066686/09.
XX

PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor

PT family ligand -
XX
XX Disclosure; Fig 13; 94pp; English.
XX

CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (570), a tumour necrosis factor-TNF
CC family ligand), having the consensus sequence, but not the extracellular region
CC of BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA cysteine-rich extracellular region.
CC
CC
SQ Sequence 58 AA;

Query Match 91.6%; Score 219; DB 23; Length 58;
Best Local Similarity 100.0%; Pred. No. 1,4e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSONEYFDSLHCIPQLRCSSNTPPLTCORCNASY 42
Db 1 CSONEYFDSLHCIPQLRCSSNTPPLTCORCNASY 38
|||||

RESULT 14
ID AAE15486 standard; peptide: 34 AA.
AAE15486:
AC AAE15486:
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX

DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
XX

KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX

OS Homo sapiens.
XX

PN WO200187979-A2.
XX

PD 22-NOV-2001.
XX

PE 14-MAY-2001; 2001WO-US15567.
XX

PF 12-MAY-2000; 2000US-204039P.
XX

PR 27-JUN-2000; 2000US-214591P.
XX

PA 14-MAY-2001; 2001US-0214591.
XX

PI (AMGE-) AMGEN INC.
XX

PI Theill LE, Yu G;
XX

WPI: 2002-066686/09.
XX

PT Inhibiting activity of B cell maturation protein and/or transmembrane

PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX
 PS Claim 1; Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein cysteine-rich consensus region.
 XX
 SQ Sequence 34 AA:
 Query Match 84.18; Score 201; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 CSQNEFYDSLHACIPQCLRCSSNTPLTCORNC 38
 DB 1 CSQNEFYDSLHACIPQCLRCSSNTPLTCORNC 34
 RESULT 15
 AAB60700
 ID AAB60700 standard; Protein: 157 AA.
 XX
 AC AAB60700:
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJ5T535.
 XX
 KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; anilinaemia; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJ5T535.
 XX
 OS Homo sapiens.
 XX
 PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

PI Thompson J;
 XX
 XX WPI: 2001-202866/20.
 DR N-PSDB: AAF60000.
 XX
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
 PT antibody homolog
 XX
 PS Example 1; Fig 3; 59pp; English.
 XX
 CC The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAFF-R protein sequence as encoded
 CC by plasmid pJ5T535. However, this BAFF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.
 XX
 SQ Sequence 157 AA:
 Query Match 75.78; Score 181; DB 22; Length 157;
 Best Local Similarity 85.78; Pred. No. 1.7e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 6; Gaps 2;
 OY 1 MAGCSQNEFYDSLHACIPQCLRCSSNTPLTCORNCASV 42
 DB 4 MAG---QNEFYDSLHACIPQCLR---NTPLTCORNCASV 39

Search completed: November 12, 2002, 16:58:33
 Job time : 17.0429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:57:01 : Search time 5.76824 Seconds
(without alignments)
214.236 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45
Perfect score: 239
Sequence: 1 MAGCOSQNEVFDSLHACIP.....LRCSSNPPLTCQRCNASV 42

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents_AA:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67.5	28.2	166	2	US-08-810-572A-6 Sequence 6, Appl1
2	67.5	28.2	166	4	US-09-290-333-6 Sequence 6, Appl1
3	67.5	28.2	293	2	US-08-810-572A-2 Sequence 2, Appl1
4	67.5	28.2	293	4	US-09-290-333-2 Sequence 2, Appl1
5	56	23.4	2476	2	US-08-276-967-2 Sequence 2, Appl1
6	55.5	23.2	3405	4	US-08-718-388-9 Sequence 9, Appl1
7	54.5	22.8	350	2	US-08-999-811-4 Sequence 4, Appl1
8	54.5	22.8	350	2	US-08-824-996-2 Sequence 2, Appl1
9	54.5	22.8	350	3	US-09-042-105-4 Sequence 4, Appl1
10	54.5	22.8	350	4	US-08-510-133A-33 Sequence 3, Appl1
11	54.5	22.8	350	4	US-08-585-895-33 Sequence 33, Appl1
12	54.5	22.8	419	2	US-08-999-811-2 Sequence 2, Appl1
13	54.5	22.8	419	3	US-09-042-105-2 Sequence 2, Appl1
14	54.5	22.8	419	3	US-09-042-105-18 Sequence 18, Appl1
15	54.5	22.8	419	4	US-08-795-430-8 Sequence 8, Appl1
16	54.5	22.8	419	4	US-08-510-133A-35 Sequence 35, Appl1
17	54.5	22.8	419	4	US-09-355-700-8 Sequence 8, Appl1
18	54.5	22.8	419	4	US-09-355-700-58 Sequence 58, Appl1
19	54.5	22.8	419	4	US-08-601-132-33 Sequence 33, Appl1
20	54.5	22.8	419	4	US-08-706-054A-3 Sequence 3, Appl1
21	54.5	22.8	419	5	PCR-US96-09001-2 Sequence 2, Appl1
22	54	22.6	609	2	US-08-716-301-4 Sequence 4, Appl1
23	53.5	22.4	77	2	US-08-465-380-4 Sequence 4, Appl1
24	53.5	22.4	77	2	US-08-465-380-40 Sequence 40, Appl1
25	53.5	22.4	77	2	US-08-480-478-33 Sequence 33, Appl1
26	53.5	22.4	77	2	US-08-486-397-4 Sequence 4, Appl1
27	53.5	22.4	77	2	US-08-486-397-40 Sequence 40, Appl1

28	53.5	22.4	77	2	US-08-486-399-4 Sequence 4, Appl1
29	53.5	22.4	77	2	US-08-486-399-40 Sequence 40, Appl1
30	53.5	22.4	77	2	US-08-461-965-4 Sequence 4, Appl1
31	53.5	22.4	77	2	US-08-461-965-40 Sequence 40, Appl1
32	53.5	22.4	77	2	US-08-326-110A-33 Sequence 33, Appl1
33	53.5	22.4	77	2	US-08-634-641-4 Sequence 4, Appl1
34	53.5	22.4	77	2	US-08-634-641-40 Sequence 40, Appl1
35	53.5	22.4	77	3	US-09-249-471-4 Sequence 4, Appl1
36	53.5	22.4	77	3	US-09-249-471-40 Sequence 40, Appl1
37	53.5	22.4	77	3	US-09-249-472-4 Sequence 4, Appl1
38	53.5	22.4	77	3	US-09-249-472-40 Sequence 40, Appl1
39	53.5	22.4	77	3	US-09-249-451-4 Sequence 4, Appl1
40	53.5	22.4	77	3	US-09-249-451-40 Sequence 40, Appl1
41	53.5	22.4	77	3	US-08-809-455-4 Sequence 4, Appl1
42	53.5	22.4	77	3	US-08-809-455-40 Sequence 40, Appl1
43	53.5	22.4	77	3	US-09-249-461-4 Sequence 4, Appl1
44	53.5	22.4	77	3	US-09-249-461-40 Sequence 40, Appl1
45	53.5	22.4	77	3	US-09-249-448-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CANI, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-6
Query Match 28.2%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 0.61;

Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSONEYFDSLHACIPQQLRCSSNTPPLTCQRYCNA 40
1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 34 CPREQYWDPLGTCMCKTICNHQS-QRTCAACRS 68

RESULT 2
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:

APPLICANT: Bram, Richard J.
von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

CITY: Hackensack
STATE: New Jersey
COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-Apr-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 28.2%; Score 67.5; DB 4; Length 166;
Best Local Similarity 30.6%; Pred. No. 0.61;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSONEYFDSLHACIPQQLRCSSNTPPLTCQRYCNA 40
1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 34 CPREQYWDPLGTCMCKTICNHQS-QRTCAACRS 68

RESULT 3
US-08-810-572A-2

; Sequence 2, Application US/08810572A

; Patent No. 5969102

; GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-Feb-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-2

Query Match 28.2%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.6%; Pred. No. 1.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSONEYFDSLHACIPQQLRCSSNTPPLTCQRYCNA 40
1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 34 CPREQYWDPLGTCMCKTICNHQS-QRTCAACRS 68

RESULT 4
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

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QY      5 CSONEYPDSLHACIPCOLRCSNPPPTCORVCNA 40  
        I : ! : ! : ! : ! : ! : ! : ! :  
Db     34 CPEDGYWDPILGTCMSCKTICNHQS-QRTCAFAFCS 68
```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-I-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-290-333-2

Query Match 28.2% Score 67.5 DB 4 Length 293;
Best Local Similarity 30.6%; Pred. No. 1.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1.

US-08-276-967-2
Sequence 2, Application US/08276967
Patent No. 5851817
GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
APPLICANT: Gardner, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Review #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSP:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
TYPE: amino acid
STRANDEDNESS: single

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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-276-967-2

Query Match      23.4%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 1.9e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2.

QY      5 CSONEYFDSLHACIP-CQ---LRCSNTPPIATCQRYC 38
      || : : | : | : | : | : | : | : | : | : |
Db 1851 CSAHSVYTSQVPSCLPSCQDPREGQCTGAGAPSTCEGCG 1888

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RESULT 6
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-718-388-9

Query Match 23.2%; Score 55.5; DB 4; Length 5405;
Best Local Similarity 33.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2

QY 4 QCSQNEFYDSLHACT-PCQLFCSSTPTPTTCORIC 38
      : 11 : : : 1 1 1 1 : 1 1 1
Db 3933 ECPQNSHYE---LCADTCISLGSALSAPLQCPDGC 3964

RESULT 7
US-08-999-811-4
; Sequence 4, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/999,811
;; FILING DATE: HEREWITTH
;; CLASSIFICATION:
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MARKOWICZ, KAREN R.
;; REGISTRATION NUMBER: 36,351
;; REFERENCE/DOCKET NUMBER: 1488.1000004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;;
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-999-811-4

Query Match 22.8%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSQNEFYDSLHACIPQCLRCSSNPP--PLTCQRYCNAS 41
Db 258 QCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECCTES 296

RESULT 8
US-08-824-996-2
; Sequence 2, Application US/08824996B
; Patent No. 5935820
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Rosen, Craig A.
; APPLICANT: Cao, Liang
; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
; FILE REFERENCE: PFI12D1
; CURRENT APPLICATION NUMBER: US/08/824,996B
; CURRENT FILING DATE: 1997-03-27
; EARLIER APPLICATION NUMBER: 08/207,550
; EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
;;
;; US-08-824-996-2

Query Match 22.8%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSQNEFYDSLHACIPQCLRCSSNPP--PLTCQRYCNAS 41
Db 258 QCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECCTES 296

RESULT 9
US-09-042-105-4
; Sequence 4, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITTH
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;;
;; US-09-042-105-4

Query Match 22.8%; Score 54.5; DB 3; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSQNEFYDSLHACIPQCLRCSSNPP--PLTCQRYCNAS 41
Db 258 QCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECCTES 296

RESULT 10
US-08-510-133A-33
; Sequence 33, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
; APPLICANT: Allitalo, Karl

;; Joukov, Vladimir
;; TITLE OF INVENTION: Receptor Ligand
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/510,133A
;; FILING DATE: 01-Aug-1995
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gass, David A.
;; REGISTRATION NUMBER: 38,153
;; REFERENCE/DOCKET NUMBER: 28113/32863
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;;
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-510-133A-33
;
Query Match 22.8%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
;
QY 4 OCSQNEYFDSLHACIPCOLRCSSNTP--PLTCQRYCNAS 41
DB 258 OCGANREFDENTCGCV-CKRTCPRNQPLNPGKACCECTES 296
;
RESULT 11
US-08-585-895-33
;; Sequence 33, Application US/08585895
;; Patent No. 6245530
;; GENERAL INFORMATION:
;; APPLICANT: Altalo, Karl
;; APPLICANT: Joukov, Vladimir
;; TITLE OF INVENTION: Receptor Ligand
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/585,895
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gass, David A.
;; REGISTRATION NUMBER: 38,153

;; REFERENCE/DOCKET NUMBER: 28113/33072
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-585-895-33
;
Query Match 22.8%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
;
QY 4 OCSQNEYFDSLHACIPCOLRCSSNTP--PLTCQRYCNAS 41
DB 258 OCGANREFDENTCGCV-CKRTCPRNQPLNPGKACCECTES 296
;
RESULT 12
US-08-999-811-2
;; Sequence 2, Application US/08999811
;; Patent No. 5932540
;; GENERAL INFORMATION:
;; APPLICANT: HU, JING-SHAN
;; APPLICANT: ROSEN, CRAIG A.
;; APPLICANT: CAO, LIANG
;; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/999,811
;; FILING DATE: HERewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MARKOWICZ, KAREN R.
;; REGISTRATION NUMBER: 36,351
;; REFERENCE/DOCKET NUMBER: 1488.1000004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 419 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-999-811-2
;
Query Match 22.8%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 QCSQNEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 13

US-09-042-105-2
Sequence 2, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: HU, JING-SHAN
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
SOFTWARE: PatentIn Release #1.0, Version #1.30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-2

Query Match 22.8%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 QCSQNEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 14
US-09-042-105-18
Sequence 18, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN

APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
SOFTWARE: PatentIn Release #1.0, Version #1.30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-18

Query Match 22.8%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 QCSQNEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 15
US-08-795-430-8
Sequence 8, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Alltalo, Karl
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
NUMBER OF SEQUENCES: 57
SOFTWARE: PatentIn Release #1.0, Version #1.30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-8

Query Match 22.8%; Score 54.5; DB 4; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Caps 2;

OY 4 QCSONEYEDSLHACIPQILRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQV-CKRTCPNQPILNPKCKACECTES 365

Search completed: November 12, 2002, 17:01:42
Job time : 6.76824 secs

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OM protein - protein search, using sw model

Run on: November 12, 2002, 17:00:26 : Search time 3.24464 Seconds

(without alignments)
186.640 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45

Perfect score: 239
Sequence: 1 MAGCSONEYFDSLHACIP.....LRCSNTPLTCORYCNASV 42

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications -AA:*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB pep:*
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4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB pep:*
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7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB pep:*
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14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	239	100.0	181	10	US-09-854-864-6
3	239	100.0	283	10	US-09-854-864-9
4	219	91.6	58	10	US-09-854-864-21
5	201	84.1	34	10	US-09-854-864-7
6	201	84.1	81	10	US-09-854-864-13
7	156	65.3	185	10	US-09-854-864-11
8	156	65.3	281	10	US-09-854-864-10
9	95.5	40.0	117	10	US-09-854-864-12
10	67.5	28.2	37	9	US-09-779-0504-45
11	67.5	28.2	59	10	US-09-854-864-20
12	67.5	28.2	166	10	US-09-854-864-15
13	67.5	28.2	291	9	US-09-779-0504-43
14	67.5	28.2	293	9	US-09-779-0504-42
15	67.5	28.2	293	10	US-09-879-919-22
16	67.5	28.2	293	10	US-09-854-864-14
17	67.5	28.2	293	10	US-09-961-376-2
18	67.5	28.2	397	10	US-09-854-864-18
19	66.5	27.8	67	10	US-09-854-864-16

20	64.5	27.0	418	9	US-09-886-429-2	Sequence 2, Appl
21	64.5	27.0	735	10	US-09-898-570-10	Sequence 10, Appl
22	64.5	27.0	845	10	US-09-898-570-12	Sequence 12, Appl
23	64.5	27.0	974	10	US-09-898-570-14	Sequence 14, Appl
24	64.5	27.0	1009	10	US-09-898-570-16	Sequence 16, Appl
25	59.5	24.9	3034	10	US-09-737-149-25	Sequence 25, Appl
26	59.5	24.9	3034	10	US-09-737-149-30	Sequence 30, Appl
27	59	24.7	38	9	US-09-779-0504-46	Sequence 46, Appl
28	56	23.4	162	10	US-09-798-789-10	Sequence 10, Appl
29	55.5	23.2	5405	10	US-09-922-217-1116	Sequence 1116, Ap
30	54.5	22.8	419	9	US-10-044-622-3	Sequence 3, Appl
31	54.5	22.8	419	10	US-09-795-0064-22	Sequence 22, Appl
32	54.5	22.8	419	12	US-10-127-551-2	Sequence 2, Appl
33	54.5	22.8	997	10	US-09-747-371-3	Sequence 3, Appl
34	53	22.2	131	10	US-09-790-264-61	Sequence 61, Appl
35	52	21.8	689	10	US-09-071-838-2	Sequence 2, Appl
36	51.5	21.5	136	10	US-09-893-737-302	Sequence 302, App
37	51.5	21.5	392	10	US-09-898-570-39	Sequence 39, Appl
38	51.5	21.5	999	10	US-09-747-371-2	Sequence 2, Appl
39	51	21.3	153	10	US-09-800-909-3	Sequence 3, Appl
40	51	21.3	153	10	US-09-884-987-4	Sequence 4, Appl
41	51	21.3	413	10	US-09-800-908-12	Sequence 12, Appl
42	51	21.3	161	9	US-09-898-234-4	Sequence 4, Appl
43	51	21.3	161	10	US-09-899-422-4	Sequence 4, Appl
44	51	21.3	161	10	US-09-907-263-2	Sequence 2, Appl
45	51	21.3	162	10	US-09-798-789-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-6
Sequence 6, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-6
Query Match 100.0%; Score 239; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MAGCSONEYFDSLHACIPCOLRCSNTPLTCORYCNASV 42
OY 1 MAGCSONEYFDSLHACIPCOLRCSNTPLTCORYCNASV 42
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
TITLE OF INVENTION: BLYS/AGP-3, AND TACI

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; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match
Best Local Similarity 100.0%; Score 239; DB 10; Length 181;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGCQSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 42
Db 1 MAGCQSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 42

RESULT 3
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match
Best Local Similarity 100.0%; Score 239; DB 10; Length 283;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGCQSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 42
Db 1 MAGCQSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 42

RESULT 4
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match
Best Local Similarity 91.6%; Score 219; DB 10; Length 58;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 42
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 38

RESULT 5
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match
Best Local Similarity 84.1%; Score 201; DB 10; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 38
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORCYNASV 34

RESULT 6
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13
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Query Match 84.1%; Score 201; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CSQNEFYDSLHACIPCOLRCSSNTPPLTCQRYC 38
DB 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 7

US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 65.3%; Score 156; DB 10; Length 185;
Best Local Similarity 69.0%; Pred. No. 7e-12;
Matches 29; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 1 MAGCCSONEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 42
DB 1 MAGCCSONEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 40

RESULT 8

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 65.3%; Score 156; DB 10; Length 281;
Best Local Similarity 69.0%; Pred. No. 1e-11;
Matches 29; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 1 MAGCCSONEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 42
DB 1 MAGCCSONEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 40

DB 1 MAGCCSONEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 40

RESULT 9

US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 40.0%; Score 95.5; DB 10; Length 117;
Best Local Similarity 63.9%; Pred. No. 6.4e-05;
Matches 23; Conservative 3; Mismatches 3; Indels 7; Gaps 4;

QY 6 SONEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 41
DB 2 AQCCEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 30

RESULT 10

US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-45

Query Match 28.2%; Score 67.5; DB 9; Length 37;
Best Local Similarity 30.6%; Pred. No. 0.044;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSQNEFYDSLHACIPCOLRCSSNTPPLTCQRYCNASV 40
DB 2 CPEQYWDPLGTGCMSCCTICNHQS-ORTCAAFCRS 36

RESULT 11

US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match      28.2%; Score 67.5; DB 10; Length 59;
Best Local Similarity 30.6%; Pred. No. 0.068;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      5 CSONEYFDSLHACIPQALRCSSNTPLTCQRCNA 40
DB      1 CPBEQYWDPLGTGCMSCRTICNHQS-ORTCAFCRS 35

RESULT 12
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      28.2%; Score 67.5; DB 10; Length 166;
Best Local Similarity 30.6%; Pred. No. 0.18;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      5 CSONEYFDSLHACIPQALRCSSNTPLTCQRCNA 40
DB      34 CPBEQYWDPLGTGCMSCRTICNHQS-ORTCAFCRS 68

RESULT 13
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match      28.2%; Score 67.5; DB 9; Length 291;
Best Local Similarity 30.6%; Pred. No. 0.31;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      5 CSONEYFDSLHACIPQALRCSSNTPLTCQRCNA 40
DB      34 CPBEQYWDPLGTGCMSCRTICNHQS-ORTCAFCRS 68

RESULT 14
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match      28.2%; Score 67.5; DB 9; Length 293;
Best Local Similarity 30.6%; Pred. No. 0.31;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      5 CSONEYFDSLHACIPQALRCSSNTPLTCQRCNA 40
DB      34 CPBEQYWDPLGTGCMSCRTICNHQS-ORTCAFCRS 68

RESULT 15
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:36 ; Search time 6.48927 Seconds

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Title: US-09-848-271-2_COPY_4_45

Perfect score: 239

Sequence: 1 MAGCCSONEYFDSLHACIPCRCSNTPPLTCQRCNASV 42

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Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	100.0	184	2	S43486 B-cell maturation
2	69.5	29.1	1548	2	S34583 serine proteinase
3	69.5	29.1	5376	2	T42215 zonadhesin - mouse
4	66	27.6	1101	2	T16840 hypothetical prote
5	61.5	25.7	1299	2	T43251 furin (EC 3.4.21.7
6	59.5	24.9	3034	2	T14119 seven-pass transme
7	59	24.7	330	2	T25169 hypothetical prote
8	59	24.7	758	2	T15577 hypothetical prote
9	59	24.7	1717	1	A45558 epidermal growth f
10	58	24.3	63	2	S07127 chymotrypsin/elast
11	58	24.3	1513	2	T23681 hypothetical prote
12	57.5	24.1	1680	2	A43434 furin (EC 3.4.21.7
13	57	23.8	502	2	T20130 hypothetical prote
14	57	23.8	653	2	G96675 hypothetical prote
15	57	23.8	838	2	T20125 hypothetical prote
16	56.5	23.6	99	2	S60231 zonadhesin - regula
17	56	23.4	2476	2	T34022 hypothetical prote
18	56	23.4	2824	2	T22759 hypothetical prote
19	55.5	23.2	989	2	T01519 hypothetical prote
20	55	23.0	1620	2	T27283 hypothetical prote
21	54.5	22.8	392	2	T27303 hypothetical prote
22	54.5	22.8	419	2	S69207 vascular endotheli
23	54.5	22.8	2155	2	T30197 alpha tectorin - m
24	54	22.6	497	2	T27827 MEG6 protein - ra
25	54	22.6	1574	2	T13954 myosin heavy chain
26	54	22.6	1980	2	S54307 myosin-1xb [simila
27	54	22.6	2022	2	A59256 hypothetical prote
28	53.5	22.4	255	2	A84544 finger protein YUL
29	53.5	22.4	758	2	S46625

30	53.5	22.4	915	2	T21773 hypothetical prote
31	53.5	22.4	927	2	T21772 hypothetical prote
32	53	22.2	274	2	F86276 P14117.2 protein -
33	53	22.2	294	2	T23682 hypothetical prote
34	53	22.2	592	1	UC1480 protein kinase C (
35	52.5	22.2	596	2	F88188 protein C18H9.7 (1
36	52.5	22.0	118	2	S61051 hypothetical prote
37	52.5	22.0	389	2	T29488 hypothetical prote
38	52.5	22.0	847	2	D72860 viral capsid assoc
39	52	21.8	56	2	JN0380 trypsin inhibitor
40	52	21.8	304	1	JC2264 tissue factor path
41	52	21.8	547	2	T34318 hypothetical prote
42	52	21.8	689	2	T52060 protein MED6A (lmp
43	52	21.8	1077	2	T41146 probable cysteine-
44	52	21.8	1474	2	D88550 protein zc84.6 (lm
45	52	21.8	1483	2	S30015 hypothetical prote

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N:Alternate names: BCM protein; BCM protein; BEL protein
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence, revision 27-Jan-1995 #text, change 21-Jul-2000
C:Accession: S43486; S31208; S36661
R:Laabl, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A:Title: The BCM gene, preferentially expressed during B lymphoid maturation, is b1c
A:Reference number: S43486; MIM:94218235; PMID:8165126
A:Accession: S43486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LAAS>
A:Cross-references: EMBL:Z29574; NID:9471244; PIDN:CA82690.1; PID:9471245
R:Laabl, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(
A:Reference number: S31208; MIM:93010984; PMID:1396583
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LA2>
A:Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:929408
A:Accession: S36661
A:Status: preliminary
A:Molecule type: RNA
A:Residues: 4-184 <LA3>
A:Cross-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCMA
A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 44/1; 93/71
C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 239; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGCCSONEYFDSLHACIPCRCSNTPPLTCQRCNASV 42
DB 4 MAGCCSONEYFDSLHACIPCRCSNTPPLTCQRCNASV 45

RESULT 2
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence, revision 10-Nov-1995 #text, change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murekaml, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:DJ7583; NID:q407344; PIDN:BA04507.1; PID:dl005033; PID:q440374
C:Keywords: hydrolase; serine proteinase

Query Match 29.1%; Score 69.5; DB 2; Length 1548;
Best Local Similarity 36.8%; Pred. No. 2; 8; Mismatches 14; Indels 5; Gaps 1;
Matches 14; Conservative 5; Mismatches 14; Indels 5; Gaps 1;

Qy 4 QCSQNEFYDLSLHACIPCOLRCSNTPP-----LTCOR 36
Db 1151 ECAVEYWDGSHRCQCHKKSCRCSPEDOCYTCR 1188
f

RESULT 3
T42215

zonadhesin - mouse
N:Alternate names: sperm-specific membrane protein
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T42215
R:Caio, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998

A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro
A:Reference number: Z22080; MUID:98133114; PMID:9452463
A:Accession: T42215
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5376 <GAO>
A:Cross-references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC26680.1
C:Genetics:
A:Gene: zan
A:Map position: 5
C:Function:
A:Description: functions in multiple cell adhesion processes
A:Note: found exclusively on the apical region of the sperm head
C:Keywords: cell adhesion

Query Match 29.1%; Score 69.5; DB 2; Length 5376;
Best Local Similarity 36.8%; Pred. No. 8;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 4 QCSQNEFYDLSLHACIPCOLRCSNTPP-----LTCOR 38
Db 3299 QCPNYSQFTDCLPSCVPCSCNRCVTPSPVSSCREGC 3336

RESULT 4
T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16840
R:Gelisel, C.

submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11101 <GET>
A:Cross-references: EMBL:U39644; NID:q1049339; PID:q1049343; PIDN:AAA0360.1; CESP:T10E1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/3; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 27.6%; Score 66; DB 2; Length 1101;

Best Local Similarity 39.4%; Pred. No. 5.4;
Matches 13; Conservative 7; Mismatches 11; Indels 2; Gaps 1;
Qy 4 QCSQNEFYDLSLHACIPCOLR--CSSNTPPLTC 34
Db 350 QCSQSTVFNSDLNVCYPLAIONCSDSSTQOPVC 382

RESULT 5
T43251

furin (EC 3.4.21.75) - fall armyworm

N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; se
C:Species: Spodoptera frugiperda (fall armyworm)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43251
R:Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A:Description: Cloning and functional characterization of FURIN from Spodoptera frugi
A:Reference number: Z22368
A:Accession: T43251
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1299 <CIE>

A:Cross-references: EMBL:Z68888; NID:q1167859; PID:z219690; PIDN:CAA93116.1
A:Experimental source: clone fstin 6; ovary
C:Function:
A:Description: responsible for the endoproteolytic processing of proproteins with spe
C:Keywords: hydrolase; serine proteinase

Query Match 25.7%; Score 61.5; DB 2; Length 1299;
Best Local Similarity 37.5%; Pred. No. 20;
Matches 15; Conservative 6; Mismatches 10; Indels 9; Gaps 3;

Qy 5 CSQNEFYDLSLHACIPCOLRCS-----SNTPPLTCORCN 39
Db 1150 CSRPLRIDLRLNOCVPC---CSERGVTNSTPPTDC-CHCN 1185

RESULT 6
T14119

seven-pass transmembrane receptor protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14119
R:Radjantonakis, A.K.; Forrester, C.J.; Little, P.F.R.

submitted to the EMBL Data Library, October 1997
A:Description: The Celser family of novel evolutionarily conserved seven-pass transmem
A:Reference number: Z17881
A:Accession: T14119
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3034 <HAD>
A:Cross-references: EMBL:AF031572; NID:g3800735; PID:g3800736; PIDN:AAC68836.1
C:Genetics:
A:Gene: Celser1
A:Map position: 15
C:Keywords: transmembrane protein
F:1-26/Domain: signal sequence #status predicted <Sig>
F:27-3034/Product: seven-pass transmembrane receptor protein #status predicted <Mat>

Query Match 24.9%; Score 59.5; DB 2; Length 3034;
Best Local Similarity 28.6%; Pred. No. 71;
Matches 14; Conservative 4; Mismatches 18; Indels 13; Gaps 2;

Qy 4 QCSQNEFYDLSLHACIPCOLR-----RCSSNTPPLTCQ-----RYCN 39
Db 2001 QCKENYKPPADACLPCCDFPHGSHSRACDMDTGQACAPGVYGRCCN 2049

RESULT 7
T25169

hypothetical protein T23F1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25169
R:Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19990
A:Accession: T25169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-330 <WT>
A:Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1
A:Experimental source: clone T23F1
C:Genetics:
A:Gene: CESP:T23F1.6
A:Map position: 5
A:Introns: 16/3
C:Superfamily: g1iad1n

Query Match	24.7%	Score 59	DB 2	Length 330
Best Local Similarity	28.9%	Pred. No. 13		
Matches	13	Conservative	7	Mismatches 17; Indels 8; Gaps 2
QY	5	CSONEYFDSLHACIP-----CQLGCSSTPTPL---TCGRYCNAS	41	
Db	59	CASSOYOLOQTSQCMPCACQSCSGCCSTNTNCTCCQCCQSCQTS	103	

RESULT 8
T11577
hypothetical protein C23G10.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T11577

Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C23610.
 A:Reference number: Z18372
 A:Accession: J15577
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-758 (<L>AT>
 A:Residues: 1-758 (<L>AT>

C:Genetics:					
A:Gene: CESP:C23G10.8					
A:Introns: 47/3: 237/3: 293/2: 405/3: 487/1: 577/3: 694/3					
C:Superfamily: Caenorhabditis elegans hypotheical protein C23G10.8					
Query Match	24.7%	Score 59:	DB 2:	Length 756:	
Best Local Similarity	42.9%	Pred. No. 25:			

```
QY      12  DSLHACIPCOLRCSSNTPPL 32
          :|: | | :|:|:|:| |
Db      260  ESVFHPPLYPAEIRCSADGPPL 280
```

RESULT 9
A4558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)

CN-specimens: Schistosoma mansoni
C.Species: Schistosoma mansoni
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A4558; S27836
R.Shoemaker, C.B., Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A.Title: Alternative splicing of the Schistosoma mansoni gene encoding a hsp70
A.Reference number: A4558; MWID:92365577; PMID:1501637

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SHO>
A:Cross-references: EMBL:M863396, NTD:g160957, PIDD:AAA29866.1, PIDD:g160956
A:Note: Sequence extracted from NCBI Backbone (NCBI:P.111129)
C:Genetics:

A:Gene: SER
C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homolog 1
E:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-171/Product: epidermal growth factor receptor homolog 1 #status predicted <MAN>
F:1018-1323/Domain: protein kinase homology 1
F:1018-1034/Region: protein kinase ATP-binding motif
F:1026-1026/Region: protein kinase ATP-binding motif

	Query Match	Similarity	Score	DB	Length
Best Local	39.1%	Pred. No.	50		
Matches	9	Conservative	3	Mismatches	11
				Indels	0
				Gaps	0
OY	4	OCSONEYFDSLHACIPCQLRCS	26		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
DB	645	ECPRNTYIDPOTRHICIPNESCS	667		

RESULT 10
S07127
chymotrypsin/elastase inhibitor - common roundworm
C.Species: Ascaris lumbricoides (common roundworm)
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C.Accession: S07127

Arch. Biochem. Biophys. 232, 143-161, 1984
A:Title: The isoinhibitors of chymotrypsin/elastase from *Ascaris lumbricoides*: the p
A:Reference number: S07127; MUID:84255715; PMID:6564898
A:Accession: S07127
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <BAB>

Query Match	24.3%	Score 58	DB 2	Length 63	
Best Local Similarity	36.6%	Pred. No. 4.1			
Matches	15	Conservative	5	Mismatches 13	
				Indels 8	
				Gaps 4	
OY	5	CSONEYFDSLHACIPQALRC	--SSNTP	-PIPLQQR	YCNAS 41
	1	1	1	1	1
	1	1	1	1	1
	1	1	1	1	1
Db	5	CGPNVEWYTE---	CTGCCEMKCGPDEDT	PCPLMLKRCSCGCS	41

RESULT 11
T23681
hypothetical protein M02G_1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 15-Oct-1999
C:Accession: T23681

A;Reference number: Z19781
A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DD

A;Residues: 1-1513 <MIL>
A;Cross-references: EMBL:281573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02G9.1
A;Experimental source: clone M02G9
C;Genetics:

A: Gene: CEST-M02637.1
A: Map position: 2
A: Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
Query Match 24.3%; Score 58; DB 2; Length 1513;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 14; Conservative 3; Mismatches 13; Indels 2;

97	12	SOLUBLE LOGIC DON'T LOGIC	4
		:	
D6	141	DSQMCNQNCQACVQSNSPPAYCQOQCROS	172
		:	
RESULT 12			
A43434			

furlin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
 C:Accession: A43434
 R:Reborek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dunke, U.; Rentrop, M.; Gateff, E.
 J. Biol. Chem. 267, 17208-17215, 1992
 A:Title: Cloning and functional expression of Dfurlin2, a subtilisin-like proprotein proc
 A:Reference number: A43434; MUID:92381036; PMID:1512259
 A:Accession: A43434
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1680 <ROE>
 A:Cross-references: GB:M94375; NID:g157461; PID:g157462
 A:Note: Sequence extracted from NCBI backbone (NCBIN:111933, NCBI:P.111934)
 C:Genetics:
 A:Gene: FlyBase:Fur2
 A:Cross-references: FlyBase:F8gn0004598
 C:Superfamily: subtilisin homology
 C:Keywords: hydrolase; serine proteinase; transmembrane protein
 F:409-652/Domain: subtilisin homology <SFT>
 F:418-457/Active site: Asp, His, Ser #status predicted

Query Match 24.1%; Score 57.5; DB 2; Length 1680;
 Best Local Similarity 34.3%; Pred. No. 74;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

OY 5 CSQNEFYDSLHACIPQLRCSN-NTPLTCORYC 38
 Db 1199 CSESEFYSGVGGCRPCGSCGSCNPADTSC 1233

RESULT 13
 T20130
 hypothetical protein C50H2.3b - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20130
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19226
 A:Accession: T20130
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-502 <WTL>
 A:Cross-references: EMBL:Z73971; PIDN:CAA98256.1; GSPDB:GN00023; CESP:C50H2.3b
 A:Experimental source: clone C50H2
 C:Genetics:
 A:Gene: CESP:C50H2.3b
 A:Map position: 5
 A:Introns: 72/1; 122/1; 152/3; 188/1; 209/1; 255/1; 301/1; 339/1; 424/1

Query Match 23.8%; Score 57; DB 2; Length 502;
 Best Local Similarity 34.7%; Pred. No. 31;
 Matches 17; Conservative 5; Mismatches 15; Indels 12; Gaps 3;

OY 1 MAGCCSNEYFDSLHACIPQL-----RCSSNT-----PPLTCORCNA 40
 Db 70 MNGQMOQRYYFD--HASLTCROFDFGCRSDSRNIFDELTCOMLCES 115

RESULT 14
 G96675
 hypothetical protein T23K8.9 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: G96675
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96675
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-653 <STO>
 A:Cross-references: GB:AE005173; NID:g4646199; PIDN:AMD26872.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T23K8.9
 A:Map position: 1

Query Match 23.8%; Score 57; DB 2; Length 653;
 Best Local Similarity 38.9%; Pred. No. 38;
 Matches 14; Conservative 3; Mismatches 13; Indels 6; Gaps 2;

OY 3 GQCS--ONEYFDSLHACIPC---QLRCSNTPPL 32
 Db 194 GNCSLCGKKIFDEMFRHCSACNFTLDRCVSLPPL 229

RESULT 15
 T20125
 hypothetical protein C50H2.3a - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20125
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19226
 A:Accession: T20125
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-838 <NTL>
 A:Cross-references: EMBL:Z73971; PIDN:CAA98251.1; GSPDB:GN00023; CESP:C50H2.3a
 A:Experimental source: clone C50H2
 C:Genetics:
 A:Gene: CESP:C50H2.3a
 A:Map position: 5
 A:Introns: 31/1; 98/1; 162/1; 199/1; 244/1; 279/1; 323/1; 354/2; 391/1; 408/1; 458/1;

Query Match 23.8%; Score 57; DB 2; Length 838;
 Best Local Similarity 34.7%; Pred. No. 47;
 Matches 17; Conservative 5; Mismatches 15; Indels 12; Gaps 3;

OY 1 MAGCCSNEYFDSLHACIPQL-----RCSSNT-----PPLTCORCNA 40
 Db 406 MNGQMOQRYYFD--HASLTCROFDFGCRSDSRNIFDELTCOMLCES 451

Search completed: November 12, 2002, 17:01:04
 Job time: 8.48927 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:49:26 : Search time 3.60515 Seconds

(without alignments)
483.199 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45

Sequence: 1 MAGQCSQNFYFSLHACIP.....LRCSSNTPTTCRCYCNASV 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	239	100.0	184	1	Q02223 homo sapien
2	156	65.3	185	1	TR17_MOUSE
3	71.5	29.9	249	1	TR13_MOUSE
4	69.5	29.1	1877	1	PKC5_MOUSE
5	69.5	29.1	5376	1	ZAN_MOUSE
6	67.5	28.2	293	1	TR13_MOUSE
7	63	26.4	175	1	TR13_MOUSE
8	62	25.9	1592	1	SORL_CHICK
9	60	25.1	867	1	SPO_BOVIN
10	59.5	24.9	3034	1	CLRI_MOUSE
11	58	24.3	63	1	ICEL_ASCSU
12	57.5	24.1	1680	1	FUR2_DROME
13	57	23.8	708	1	YB40_HUMAN
14	56.5	23.6	99	1	GAS3_ARATH
15	56	23.4	2476	1	ZAN_PIG
16	55	23.0	760	1	EZ_DROME
17	54.5	22.8	419	1	VEGC_HUMAN
18	54	22.6	1980	1	MY9B_RAT
19	54	22.6	2114	1	MY9B_MOUSE
20	54	22.6	2158	1	MY9B_HUMAN
21	53.5	22.4	381	1	P53_CANFA
22	53.5	22.4	758	1	YJ06_YEAST
23	53	22.2	131	1	ALKI_MOUSE
24	53	22.2	591	1	KPC2_RABIT
25	53	22.2	592	1	KPC2_MOUSE
26	52.5	22.0	323	1	TNR6_BOVIN
27	52.5	22.0	847	1	Y083_NPAC
28	52	21.8	56	1	ITR4_RADMA
29	52	21.8	304	1	TEPI_MACMU
30	52	21.8	470	1	PROP_CAYPO
31	52	21.8	1483	1	UFDA_YEAST
32	52	21.8	1696	1	PKC5_BRACL
33	51.5	21.5	63	1	AMP2_MIRJA

34	51.5	21.5	701	1	YAB5_SCHPO	009807 schizosach
35	51.5	21.5	1935	1	YBBA_SCHPO	060072 schizosach
36	51.5	21.5	3695	1	LMAS_HUMAN	015220 homo sapien
37	51	21.3	183	1	Y189_ACTIS	093887 actinobact
38	51	21.3	455	1	TR1A_HUMAN	P19438 homo sapien
39	51	21.3	592	1	KPC2_RAT	09x021 ratius norv
40	51	21.3	1062	1	NAL2_HUMAN	09x02 homo sapien
41	51	21.3	3718	1	LMAS_MOUSE	061001 mus musculu
42	50.5	21.1	100	1	KRP2_COLLI	093499 columba liv
43	50.5	21.1	610	1	C4BP_BOVIN	028065 bos taurus
44	50.5	21.1	1013	1	PRML_DROME	P82295 drosophila
45	50.5	21.1	3014	1	CLRI_HUMAN	09ny96 homo sapien

ALIGNMENTS

RESULT 1	TR17_HUMAN	STANDARD:	PRT:	184 AA.
ID	TR17_HUMAN			
AC	Q02223			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).			
GN	TNFRSF17 OR BCMA OR BCM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND CHROMOSOMAL TRANSLOCATION.			
RC	TTSUDE-Peripheral blood leukocytes, and Lymph node;			
MD	MDLINE=93010984; PubMed=1396583;			
RA	Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";			
RL	EMBO J. 11:3897-3904(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MDLINE=94218235; PubMed=8165126;			
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";			
RL	Nucleic Acids Res. 22:1147-1154(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MDLINE=99425270; PubMed=10493829;			
RA	Loftus B.J., Kim U.-J., Smedson V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Elchler E.E., Harris P.C., Venter J.C., Adams M.D.;			
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";			
RL	Genomics 60:295-308(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. AND VARIANT THR-153.			
RC	MDLINE=21419161; PubMed=11528522;			
RA	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;			
RT	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";			
RL	Genes Immun. 2:276-279(2001).			
RN	[5]			
RP	FUNCTION.			
RC	MDLINE=20363816; PubMed=10903733;			
RA	Hatzoglou A., Rousset J., Bourgaud M.-F., Rogier E., Madry C., Inoue J., Devergne O., Tsapis A.;			
RT	"TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38			

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.;
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RT Nature 404:995-999(2000).
 RL [7]
 RN FUNCTION AND INTERACTION WITH APRIL AND BAFF.
 RP MEDLINE=21170294; PubMed=10973284;
 RX Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sattoli I., Hsu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RT Nat. Immunol. 1:252-256(2000).
 RN [8]
 RN INTERACTION WITH TRAF5 AND TRAF6.
 RP MEDLINE=20381353; PubMed=10908663;
 RX Shu H.-B., Johnson H.;
 RA "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 CC EMBL: Z14954; CAA78679.1; -;
 DR EMBL: Z29575; CAA82691.1; -;
 DR EMBL: Z29574; CAA82690.1; -;
 DR EMBL: U95742; AAB67251.1; -;
 DR EMBL: AB052772; BAB60895.1; -;
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Genew: HGNC:11913; TNFRSF17.
 KM MIM: 109545; -;
 KW Receptor: Immune response; Proto-oncogene; Signal-anchor;
 KM Receptor: Chromosomal translocation: Polymorphism.
 FT DOMAIN 1 54
 FT TRANSMEM 53 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT TNFR-CYS.
 FT SITE 3 4
 FT BREAKPOINT FOR TRANSLOCATION TO FORM
 FT INTERLEUKIN 2/BCM ONCOGENE.
 FT BY SIMILARITY.
 FT DISULFID 8 21
 FT DISULFID 24 37
 FT DISULFID 28 41
 FT VARIANT 153 153
 FT A -> T.
 FT /FTID-VAR_012234
 SQ SEQUENCE 184 AA; 20138 MW; 277AF1E2767D932 CRC64;

Query Match 100.0%; Score 239; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MAGGCSQNEFFDSILHACIPQALRGSSNTPPTLCORCNASV 42
 Db 4 MAGGCSQNEFFDSILHACIPQALRGSSNTPPTLCORCNASV 45
 ||||||||||||||||||||||||||||||||||||||||||||
 RESULT 2
 ID TR17_MOUSE STANDARD: PRT; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RP SRRAIN-BALB/C; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Medry C., Laabl Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC SRRAIN-C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Friesemann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 or send an email to license@lstb-sib.ch).

DR EMBL: AF061505; AAC23799.1; -;
 DR EMBL: AK020247; BAB32038.1; -;
 DR MGI: MGI:1343050; Tnftrsf17.
 KM Receptor: Immune response; Signal-anchor; Transmembrane;
 KM Alternative splicing
 FT DOMAIN 1 49
 FT TRANSMEM 50 70
 FT
 FT DOMAIN 71 185
 FT REPEAT 4 36
 FT DISULFID 5 18
 FT DISULFID 21 32
 FT DISULFID 25 36
 FT VARSPLIC 87 91
 FT SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 65.3%; Score 156; DB 1; Length 185;
 Best Local Similarity 69.0%; Pred. No. 1.7e-12;
 Matches 29; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy 1 MAGCSONEYFDSLHACIPQRLCSSNTPPLFCORCYCASV 42
 Db 1 MAGCSEYFDSLHACRCHLRCNS--PPATCPCYCDPSV 40

RESULT 3
 T13X_MOUSE STANDARD; PRT; 249 AA.

AC 09ET35; Q9DBZ3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TNF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RX MEDLINE-21177254; PubMed-10881172;
 RA Van M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 RA Dixit V.M.;
 RT "Identification of a receptor for Blys demonstrates a crucial role in
 RT humoral immunity.";
 RL Nat. Immunol. 1:37-41(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-Lung;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staudil P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Brownstein M.J., Bult C., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzei J.J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE-20341628; PubMed-10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovoyev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stollina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Hsu H.;
 RT "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE-21322748; PubMed-11429548;
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Van M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TAC1-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice.";
 RL Nat. Immunol. 2:632-637(2001).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (By
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLg with its C-terminus (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS

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DR EMBL: AF257673; AAC00081.1; -;
 DR EMBL: AK004668; BAB23457.1; -;
 DR MGI: MGI:1889411; Tnftrsf13b.
 DR PROSITE: PS00652; TNFR_NCFR1; 1.
 DR PROSITE: PS50050; TNFR_NCFR2; 2.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1 128
 FT TRANSMEM 129 149
 FT
 FT DOMAIN 150 249
 FT REPEAT 5 38
 FT REPEAT 42 76
 FT DISULFID 6 19
 FT DISULFID 22 34
 FT DISULFID 26 38
 FT DISULFID 43 58
 FT DISULFID 61 72
 FT DISULFID 65 76
 FT CONFLICT 137 137
 FT SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 29.9%; Score 71.5; DB 1; Length 249;
 Best Local Similarity 35.3%; Pred. No. 0.055;
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 5 CSONEYFDSLHACIPQRLCSSNTPPLFCORCYCASV 38
 Db 6 CPKQYWDSSKSCVSCALTCORS-ORTCTDFC 38

RESULT 4
 PCKS_MOUSE STANDARD; PRT; 1877 AA.

AC 004592; 062040;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (PC 3.4.21.-)
 DE (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
 DE (Convertase PC5) (PC6) (Subtilisin-like proprotein convertase 6)
 DE (SPC).
 GN PCSK5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI-TaxId=10090;
 RN [1]
 RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).
 RC STRAIN=ICR; TISSUE=Intestine;
 RX MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT Identification of an isoform with an extremely large Cys-rich region
 of PC6, a kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PC5A).
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT Identification and functional expression of a new member of the
 mammalian kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PC5A).
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=93342056; PubMed=8341687;
 RA Lusson J., Vieu P., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 candidate proprotein convertase expressed in endocrine and
 RT nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT The isoforms of proprotein convertase PC5 are sorted to different
 RT subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calton M., Robertson E.J.;
 RT SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 RT morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like protease SPC6 is expressed during embryonic
 RT implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION: TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROTEIN SUBSTRATE BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO

CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PC5B/LONG (SHOWN HERE)
 CC AND PCSA/SHORT: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 CC ABUNDANT IN THE INTESTINE AND ADRENALS. PC5B IS EXPRESSED IN THE
 CC INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE LIPS AND THE LIVER,
 CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 CC E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 CC E7.5, INTENSE EXPRESSION IN EXTRAMEMBRYONIC ENDODERM, AMNION AND
 CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 CC SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN
 CC E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CC CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 CC TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
 CC STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CC CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
 CC ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 CC ISOFORM B OCCUR AT E12.5.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 CC WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
 CC -----
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D17583; BAA04507.1; -
 CC EMBL: D12619; BAA02143.1; -
 CC EMBL: L14932; AA474636.1; -
 CC PIR: JX0248; JX0248.
 CC PIR: A48225; A48225.
 CC HSSP: Q99405; 1MPT.
 CC MEROPS: S08.076; -.
 CC MGD: MGI:97515; PCSK5.
 CC InterPro: IPR000561; PCSK5.
 CC InterPro: IPR002174; Furin-like.
 CC InterPro: IPR002884; P_domain.
 CC InterPro: IPR000209; Peptidase_S8.
 CC Pfam: PF00082; Peptidase_S8; 1.
 CC Pfam: PF01483; P; PARTIAL.
 CC PRINTS: PR00723; SUBTILISIN.
 CC ProDom: PD000717; P_domain; 1.
 CC SMART: SM00181; EGF; 3.
 CC SMART: SM00001; EGF-like; 2.
 CC SMART: SM00261; Fv; 22.
 CC PROSITE: PS00136; SUBTILASE_ASP; 1.
 CC PROSITE: PS00137; SUBTILASE_HIS; 1.
 CC PROSITE: PS00138; SUBTILASE_SER; 1.
 CC Hydroxase: serine protease; Glycoprotein; Zymogen; Signal;
 CC Cleavage on pair of basic residues; Repeat; Alternative splicing;
 CC Transmembrane.
 CC FT SIGNAL. 1 34
 CC FT PROPEP. 35 116
 CC FT CHAIN. 117 1877
 CC FT
 CC FT DOMAIN. 117 1768
 CC FT TRANSMEM. 1769 1789
 CC FT DOMAIN. 1790 1877
 CC FT DOMAIN. 117 452
 CC FT DOMAIN. 464 602
 CC
 CC PROTEIN CONVERTASE SUBTILISIN/KEXIN
 CC TYPE 5.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC CATALYTIC.
 CC HOMO B.

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FT DOMAIN 638 1753 CYS-RICH MOTIF (CRM) REGION.
FT DOMAIN 1825 1844 AC 1.
FT DOMAIN 1856 1877 AC 2.
FT SITE 521 523 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT ACT_SITE 173 523 CELL ATTACHMENT SITE (POTENTIAL).
FT ACT_SITE 214 523 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 388 523 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 383 383 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 754 754 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 804 804 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 854 854 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 951 951 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1016 1016 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1220 1220 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1711 1711 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1733 1733 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPIC 878 915 GEYIDQGCQTCGSCACKMGPTDSCPTRYLD ->
FT VARSPIC ATEESWAGCFMVLKKNMLCQKRYLDQLCCKTCTFGG
FT VARSPIC (IN ISOFORM PCSA).
FT VARSPIC MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; EC850E2DF20EA1C3 CRC64;

Query Match 29.1%; Score 69.5; DB 1; Length 1877;
Best Local Similarity 36.8%; Pred. No. 0.61;
Matches 14; Conservative 5; Mismatches 14; Indels 5; Gaps 1;

OY 4 OCSONEYFDSLHACIPCOLRCSNMP----LTCOR 36
Db 1480 ECAVWEYWDGSHRCOPCHKCKSCGSPSDQCTPCR 1517

RESULT 5
ZAN_MOUSE STANDARD: PRT: 5376 AA.
AC 088799; 008647;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zonadhesin precursor.
GN ZAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-98123114; PubMed-9452463;
RA Gao Z., Garbers D.L.;
RT *Species diversity in the structure of zonadhesin, a sperm-specific
RT membrane protein containing multiple cell adhesion molecule-like
RT domains.*;
RT J. Biol. Chem. 273:3415-3421(1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-97271566; PubMed-9126492;
RA Gao Z., Harumi T., Garbers D.L.;
RT *Chromosome localization of the mouse zonadhesin gene and the human
RT zonadhesin gene (ZAN).*;
RL Genomics 41:119-122(1997).
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
CC SIGNALING.
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
CC APICAL REGION OF THE SPERM HEAD.
CC -1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.

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CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
CC ZONA PELLUCIDA.
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
CC SPERMATOZOEA OR PROMOTING ADHESION TO THE OVUDUCTAL ISTHMUS.
CC -1- DOMAIN: THE WFD DOMAIN 2 MAY MEDIATE COVALENT
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTERSTITIAL MUCIN MUC2).
CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
CC -1- SIMILARITY: CONTAINS 25 WFD DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL: 097068; AAC26680.1; -
CC EMBL: U83190; AAC53125.1; -
CC MGD: MGI:106656; Zan.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR003645; FOLN.
CC InterPro: IPR000998; MAM_domain.
CC InterPro: IPR002919; TIL_Cysrich.
CC InterPro: IPR003328; TILa_Cysrich.
CC InterPro: IPR001007; WVF_C.
CC InterPro: IPR001846; WVF_D.
CC DR Pfam: PF00094; wvd; 4.
CC DR Pfam: PF00629; MAM; 3.
CC DR Pfam: PF01826; TIL; 25.
CC DR Pfam: PF02345; TILa; 2.
CC DR SMART: SM00181; EGF; 2.
CC DR SMART: SM00274; FOLN; 11.
CC DR SMART: SM00137; MAM; 2.
CC DR SMART: SM00214; WVC; 17.
CC DR SMART: SM00216; WVD; 4.
CC DR PROSITE: PS00022; EGF_1; 1.
CC DR PROSITE: PS01186; EGF_2; 18.
CC DR PROSITE: PS00740; MAM_1; FALSE_NEG.
CC DR PROSITE: PS50060; MAM_2; 3.
CC KM Signal: Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
CC Repeat.
CC FT SIGNAL 1 17
CC FT CHAIN 18 5376
CC FT DOMAIN 18 5310
CC FT TRANSMEM 5311 5337
CC FT DOMAIN 5338 5376
CC FT DOMAIN 45 210
CC FT DOMAIN 215 374
CC FT DOMAIN 377 342
CC FT DOMAIN 547 1170
CC FT DOMAIN 1171 1280
CC FT DOMAIN 1281 1669
CC FT DOMAIN 1670 2056
CC FT DOMAIN 2057 2459
CC FT DOMAIN 2460 2579
CC FT DOMAIN 2580 2699
CC FT DOMAIN 2700 2819
CC FT DOMAIN 2820 2939
CC FT DOMAIN 2940 3059
CC FT DOMAIN 3060 3179
CC FT DOMAIN 3180 3299
CC FT DOMAIN 3300 3416
CC FT DOMAIN 3417 3536
CC FT DOMAIN 3537 3656
CC FT DOMAIN 3657 3776
CC FT DOMAIN 3777 3892
CC FT DOMAIN 3893 4928
CC FT DOMAIN 4029 4148
CC FT DOMAIN 4149 4263
CC -----
CC POTENTIAL.
CC ZONADHESIN.
CC EXTRACELLULAR (POTENTIAL).
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC MAM 1.
CC MAM 2.
CC MAM 3.
CC 80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
CC (MUCIN-LIKE DOMAIN).
CC WFD 1 (PARTIAL).
CC WFD 2.
CC WFD 3.
CC WFD 4.
CC WFD 5 (PARTIAL).
CC WFD 6 (PARTIAL).
CC WFD 7 (PARTIAL).
CC WFD 8 (PARTIAL).
CC WFD 9 (PARTIAL).
CC WFD 10 (PARTIAL).
CC WFD 11 (PARTIAL).
CC WFD 12 (PARTIAL).
CC WFD 13 (PARTIAL).
CC WFD 14 (PARTIAL).
CC WFD 15 (PARTIAL).
CC WFD 16 (PARTIAL).
CC WFD 17 (PARTIAL).
CC WFD 18 (PARTIAL).
CC WFD 19 (PARTIAL).

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FT DOMAIN 4264 4283 WMD 20 (PARTIAL).
FT DOMAIN 4384 4503 WMD 21 (PARTIAL).
FT DOMAIN 4504 4623 WMD 22 (PARTIAL).
FT DOMAIN 4624 4743 WMD 23 (PARTIAL).
FT DOMAIN 4744 4863 WMD 24 (PARTIAL).
FT DOMAIN 4864 5261 WMD 25.
FT DOMAIN 5259 5295 EGF-Like.
FT DISULFID 5263 5274 BY SIMILARITY.
FT DISULFID 5268 5283 BY SIMILARITY.
FT DISULFID 5285 5294 BY SIMILARITY.
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1216 1216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1314 1314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1814 1814 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1933 1933 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2028 2028 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2111 2111 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2142 2142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2332 2332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2575 2575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2692 2692 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2812 2812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3052 3052 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3065 3065 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3144 3144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3172 3172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3288 3288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3292 3292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3782 3782 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4005 4005 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4136 4136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4243 4243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4254 4254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4335 4335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4376 4376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4586 4586 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5136 5136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5252 5252 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 5376 AA; 579908 MW; 0E44DB77DF2A2620 CRC64;

Query Match 29.1%; Score 69.5; DB 1; Length 5376;
Best Local Similarity 36.8%; Pred. No. 1.6;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

OY 4 QCSQNEFYFDSLHNCIF-CQLRCSSTNP--PLTQCRYC 38
DB 3299 QCPNQSQTDLPCVPCSCNRCVETSPVSSCRGC 3336

RESULT 6
T13X_HUMAN STANDARD; PRT; 293 AA.
AC 014836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML Interactor).
GN TNFRSF13B OR TACT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA MEDLINE=97458245; Pubmed=9311921;
RA von Buehlow G.-U.; Bram R.J.;
RA "NF-AT activation induced by a CAML-interacting member of the tumor

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RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=20519647; Pubmed=10956646;
RX FUNCTION.
RX Wu Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K.,
RX Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
RX Milgrom T.S., Mardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RX Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TNFRI is a
RT high affinity receptor for TNF family members APRIL and BLYS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RX FUNCTION.
RX MEDLINE=21170294; Pubmed=10973284;
RX Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RX McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollina M.,
RX Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thiel L.E.;
RT "APRIL and TNFRI and receptors BCMA and TNFRI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TAL1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAML with its C-terminus.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the Initiator.
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CC -----
DR EMBL: AF023614; AAC51790.1; -;
DR EMBL: BC028072; AAH28072.1; -;
DR Genew: HGNC:18153; TNFRSF13B.
DR MIM: 604907; -;
DR InterPro: IPR001368; TNFR-C6.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT REPEAT 187 293 CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 67 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F9DE17A5EB CRC64;

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Query Match 28.2%; Score 67.5; DB 1; Length 293;
 Best Local Similarity 30.6%; Pred. No. 0.2;
 Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSONEYFDSLHACIPQOLFCSSNTPPLTCORYCA 40
 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
 DB 34 CPEEQYWDPLGTCMCKTCICNHQS-QRICAACFRS 68

RESULT 7
 T13C_MOUSE
 ID T13C_MOUSE STANDARD; PRT; 175 AA.
 AC Q9D8D0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3) (B-cell maturation defect).
 GN TNFRSF13C OR BAFFR OR BCMD OR BR3.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BAFB/C; TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Millan C., Struch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L., Ambrose C.;
 RT "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF".
 RL Science 293:2108-2111(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
 RC STRAIN=A/J;
 RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;
 RT "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
 RL Curr. Biol. 11:1547-1552(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka S., Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glissl C., King B., Kochiwa H., Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21614654; PubMed=11747827;
 RA Harless S.M., Lantz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K., Hilbert D.M., Hayes C.E., Cancro M.P.;

RT "Competition for Blys-mediated signaling through Bcmd/BR3 regulates peripheral B lymphocyte numbers.";
 RT Curr. Biol. 11:1986-1989(2001).
 RL [1]
 CC -1- FUNCTION: B-cell receptor specific for TNFRSF13B/TALL1/BAFF/Blys. Promotes the survival of mature B-cells and the B-cell response.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis; detected at lower levels in lung and thymus.
 CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminus. The mutant RNA is not detectable. B-cell lymphoplasia is normal, but the life span of peripheral B-cells is much reduced.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 CC DR EMBL: AF373847; AAQ91827.1; -;
 CC DR EMBL: AK008142; BAB25490.1; -;
 CC MD: MG1:1919299; TNFRSF13C.
 CC KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 CC Alternative splicing.
 CC FT DOMAIN 1 71
 CC TRANSMEM 72 92
 CC FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
 CC FT DOMAIN 93 175
 CC REPEAT 21 38
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 22 35
 CC FT BY SIMILARITY.
 CC FT CARBOHYD 27 38
 CC FT BY SIMILARITY.
 CC FT FT CARBOHYD 23 23
 CC FT N-LINKED (GICNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 133 143
 CC FT MISSING (IN ISOFORM 2).
 CC SO SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 26.4%; Score 63; DB 1; Length 175;
 Best Local Similarity 50.0%; Pred. No. 0.45;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 CSONEYFDSLHACIPQOL 23
 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
 DB 21 QCNOTCECFDPLVRNCVSCSEL 40

RESULT 8
 SORL_CHICK
 ID SORL_CHICK STANDARD; PRT; 1592 AA.
 AC Q98930;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sortilin-related receptor (Sorting protein-related receptor containing IDLR class A repeats) (SORLA) (SORLA-1) (low-density lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding repeats) (LRL1) (Fragment).
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97301565; PubMed=9157966;
 RA Morwald S., Yamazaki H., Bujo H., Kusunoki J., Kanaki T., Selmiya K., Morisaki N., Nimpf J., Schneider W.J., Saito Y.;
 RT "A novel mosaic protein containing LDL receptor elements is highly

RT conserved in humans and chickens." 992
 RL Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997). 1010
 CC -1- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT 1019
 CC MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES. 1038
 CC BINDS LDL. THE MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA, 1051
 CC AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS. BINDS THE RECEPTOR- 1060
 CC ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL 1077
 CC INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK 1099
 CC REGULATORY EFFECTS ON THIS RECEPTOR. 1099
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential). 1117
 CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN. PRESENT IN THE 1130
 CC TESTES, ADRENAL GLANDS AND DETECTABLE IN THE LUNG. 1141
 CC -1- SIMILARITY: CONTAINS 5 BNR REPEATS. 1145
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. 1155
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAINS. 1168
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. 1222
 CC ----- 1244
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration 1257
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> 1331
 CC or send an email to license@isb-sib.ch). 1351
 CC ----- 1360
 CC EMBL: Y08109; CAA69324.1; -. 6
 DR HSSP: P01130; IAUJ. 65
 DR InterPro: IPR000561; EGF-like. 275
 DR InterPro: IPR003961; FN_III. 275
 DR InterPro: IPR002860; GH_BNR. 337
 DR InterPro: IPR002172; LDL_recept_A. 337
 DR InterPro: IPR000033; LDL_receptor_rep. 523
 DR Pfam: PF00047; fn3; 1. 581
 DR Pfam: PF00057; ldl_recept_a; 11. 725
 DR Pfam: PF00058; ldl_recept_b; 5. 778
 DR Pfam: PF02012; BNR; 5. 975
 DR PRINTS: PR00261; LDLRECEPTOR. 975
 DR SMART: SM00181; EGF; 1. 1098
 DR SMART: SM00600; FN3; 1. 1098
 DR SMART: SM00192; LDLA; 11. 1152
 DR SMART: SM00135; LY; 5. 1152
 DR PROSITE: PS01186; EGF_2; 1. 1366
 DR PROSITE: PS01209; LDLA_1; 11. 1454
 DR PROSITE: PS00068; LDLA_2; 11. 1454
 KM Endocytosis: Receptor; EGF-like domain; Repeat; Glycoprotein; LDL; 1514
 KW Lipid transport; Cholesterol metabolism. 1592
 FT NON_TER 1 1592
 FT REPEAT 43 54 BNR 1. 178409 MW: 24EADA5BA231B203 CRC64;
 FT REPEAT 139 150 BNR 2. 1592
 FT REPEAT 348 359 BNR 3. 1592
 FT REPEAT 428 439 BNR 4. 1592
 FT REPEAT 469 480 BNR 5. 1592
 FT DOMAIN 710 884 5 X APPROXIMATE YWTD REPEATS. 1592
 FT REPEAT 710 713 1. 1592
 FT REPEAT 757 757 2. 1592
 FT REPEAT 798 801 3. 1592
 FT REPEAT 841 844 4. 1592
 FT REPEAT 881 884 5. 1592
 FT DOMAIN 933 979 EGF-LIKE. 1592
 FT DOMAIN 983 1021 LDL-RECEPTOR CLASS A 1. 1592
 FT DOMAIN 1022 1062 LDL-RECEPTOR CLASS A 2. 1592
 FT DOMAIN 1063 1100 LDL-RECEPTOR CLASS A 3. 1592
 FT DOMAIN 1103 1143 LDL-RECEPTOR CLASS A 4. 1592
 FT DOMAIN 1143 1180 LDL-RECEPTOR CLASS A 5. 1592
 FT DOMAIN 1180 1224 LDL-RECEPTOR CLASS A 6. 1592
 FT DOMAIN 1230 1268 LDL-RECEPTOR CLASS A 7. 1592
 FT DOMAIN 1273 1312 LDL-RECEPTOR CLASS A 8. 1592
 FT DOMAIN 1324 1362 LDL-RECEPTOR CLASS A 9. 1592
 FT DOMAIN 1376 1415 LDL-RECEPTOR CLASS A 10. 1592
 FT DOMAIN 1419 1457 LDL-RECEPTOR CLASS A 11. 1592
 FT DOMAIN 1462 1551 FIBRONECTIN TYPE-III 1. 1592
 FT DOMAIN 1559 1592 FIBRONECTIN TYPE-III 2. 1592
 FT DISULFID 985 997 BY SIMILARITY. 1592

FT DISULFID 992 1010 BY SIMILARITY. 1592
 FT DISULFID 1004 1019 BY SIMILARITY. 1592
 FT DISULFID 1024 1038 BY SIMILARITY. 1592
 FT DISULFID 1032 1051 BY SIMILARITY. 1592
 FT DISULFID 1045 1060 BY SIMILARITY. 1592
 FT DISULFID 1065 1077 BY SIMILARITY. 1592
 FT DISULFID 1072 1099 BY SIMILARITY. 1592
 FT DISULFID 1084 1099 BY SIMILARITY. 1592
 FT DISULFID 1105 1117 BY SIMILARITY. 1592
 FT DISULFID 1112 1130 BY SIMILARITY. 1592
 FT DISULFID 1124 1141 BY SIMILARITY. 1592
 FT DISULFID 1145 1155 BY SIMILARITY. 1592
 FT DISULFID 1150 1168 BY SIMILARITY. 1592
 FT DISULFID 1162 1222 BY SIMILARITY. 1592
 FT DISULFID 1232 1244 BY SIMILARITY. 1592
 FT DISULFID 1239 1257 BY SIMILARITY. 1592
 FT DISULFID 1251 1266 BY SIMILARITY. 1592
 FT DISULFID 1275 1288 BY SIMILARITY. 1592
 FT DISULFID 1283 1301 BY SIMILARITY. 1592
 FT DISULFID 1295 1310 BY SIMILARITY. 1592
 FT DISULFID 1333 1351 BY SIMILARITY. 1592
 FT DISULFID 1345 1360 BY SIMILARITY. 1592
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 581 581 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 725 725 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 778 778 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 975 975 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 1098 1098 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 1152 1152 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 1366 1366 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 1454 1454 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT CARBOHYD 1514 1514 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 FT NON_TER 1592 1592 N-LINKED (GLCNAC. .) (POTENTIAL). 1592
 SQ SEQUENCE 1592 AA: 178409 MW: 24EADA5BA231B203 CRC64; 1592

Query Match 25.9% Score 62; DB 1; Length 1592;
 Best Local Similarity 33.3% Pred. No. 4.4; 1592
 Matches 15; Conservative 6; Mismatches 18; Indels 6; Gaps 2;

Oy 3 GCGSONEYFDLSHACIP---COLR--GSSNPPYTCQRYCNAS 41
 Db 1376 GRCSPREFECQQLHKICPKNKRCGDRGCDGDENSCPHSSLS 1420

RESULT 9
 SSPO_BOVIN STANDARD; PRT; 867 AA.
 ID SSPO_BOVIN AC P98167;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE SCO-spondin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endothelium;
 RX MEDLINE=9638614; PubMed=8743952;
 RA Gobron S., Monnerie H., Weinzel R., Creveaux I., Lehmann W.,
 RA Lamalle D., Dastugue B., Weinzel A.;
 RT "SCO-spondin: a new member of the thrombospondin family secreted by
 RT the subcutaneous organ is a candidate in the modulation of neuronal
 RT aggregation.";
 RL J. Cell Sci. 109:1053-1061(1996).
 CC -1- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
 CC -1- SUBCELLULAR LOCATION: Extracellular.

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EMBL: AF031572; AAC68836.1; .

DR MGD; MGI:1100883; Celser1.

DR HSP; P00749; IURK.

DR Interpro: IPR000152; Asx_hydroxyl.

DR Interpro: IPR002126; Cadherin.

DR Interpro: IPR000561; EGF-like.

DR Interpro: IPR000832; GPCR_secretin.

DR Interpro: IPR001879; hormn_receptor.

DR Interpro: IPR002049; Laminin_Egf.

DR Interpro: IPR001791; Laminin_G.

DR Pfam: PF000203; PKD_cys-rich.

DR Pfam: PF000028; cadherin; 9.

DR Pfam: PF00008; EGF; 6.

DR Pfam: PF01825; GPS; 1.

DR Pfam: PF02793; HRM; 1.

DR Pfam: PF00053; Laminin_EGF; 1.

DR Pfam: PF00054; Laminin_G; 1.

DR PRINTS; PR00205; CADHERIN.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00112; CA; 9.

DR SMART; SM00180; EGF_Lam; 1.

DR SMART; SM00001; EGF-like; 6.

DR SMART; SM00303; GPS; 1.

DR SMART; SM00008; Hotmr; 1.

DR SMART; SM00282; Lamg; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE; PS00232; CADHERIN_1; 7.

DR PROSITE; PS0268; CADHERIN_2; 9.

DR PROSITE; PS00022; EGF_1; 6.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS0221; GPS; 1.

DR PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; FALSE_NEG.

DR PROSITE; PS00650; G-PROTEIN_RECEP_F2_3; 1.

DR PROSITE; PS0227; G-PROTEIN_RECEP_F2_4; 1.

DR PROSITE; PS0261; G-PROTEIN_RECEP_F2_4; 1.

DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.

DR PROSITE; PS0025; LAM_G_DOMAIN; 2.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;

KW Developmental protein; Hydroxylation; Signal.

FT SIGNAL 1 29

FT CHAIN 30 3034

FT DOMAIN 21 2484

FT TRANSMEM 2485 2505

FT DOMAIN 2506 2516

FT TRANSMEM 2517 2537

FT DOMAIN 2538 2542

FT TRANSMEM 2543 2563

FT DOMAIN 2564 2587

FT TRANSMEM 2588 2608

FT DOMAIN 2609 2625

FT TRANSMEM 2626 2646

FT DOMAIN 2647 2670

FT TRANSMEM 2671 2691

FT DOMAIN 2692 2694

FT TRANSMEM 2695 2715

FT DOMAIN 2716 3034

FT DOMAIN 261 368

FT DOMAIN 369 474

FT DOMAIN 475 580

FT DOMAIN 581 702

FT DOMAIN 703 804

FT DOMAIN 805 907

FT DOMAIN 908 1014

FT DOMAIN 1015 1116

FT DOMAIN 1121 1239

FT DOMAIN 1318 1376

FT DOMAIN 1378 1414

FT DOMAIN 1418 1456

FT DOMAIN 1457 1661

FT DOMAIN 1664 1700

FT DOMAIN 1704 1885

FT DOMAIN 1887 1922

FT DOMAIN 1923 1961

FT DOMAIN 1962 1994

FT DOMAIN 1996 2031

FT DOMAIN 2037 2070

FT DOMAIN 2423 2475

FT DOMAIN 2674 2678

FT DISULFID 1322 1333

FT DISULFID 1327 1364

FT DISULFID 1366 1375

FT DISULFID 1382 1393

FT DISULFID 1387 1402

FT DISULFID 1404 1413

FT DISULFID 1422 1433

FT DISULFID 1427 1443

FT DISULFID 1445 1455

FT DISULFID 1668 1679

FT DISULFID 1673 1688

FT DISULFID 1690 1699

FT DISULFID 1891 1902

FT DISULFID 1896 1911

FT DISULFID 1913 1922

FT DISULFID 1926 1937

FT DISULFID 1931 1949

FT DISULFID 1951 1960

FT DISULFID 1960 1978

FT DISULFID 1968 1981

FT DISULFID 1983 1993

FT DISULFID 2000 2015

FT DISULFID 2002 2018

FT DISULFID 2020 2030

FT MOD_RES 1681 1681

FT MOD_RES 1904 1904

FT CARBOHYD 236 236

FT CARBOHYD 561 561

FT CARBOHYD 649 649

FT CARBOHYD 793 793

FT CARBOHYD 1129 1129

FT CARBOHYD 1154 1154

FT CARBOHYD 1228 1228

FT CARBOHYD 1264 1264

FT CARBOHYD 1274 1274

FT CARBOHYD 1302 1302

FT CARBOHYD 1591 1591

FT CARBOHYD 1638 1638

FT CARBOHYD 1655 1655

FT CARBOHYD 1994 1994

FT CARBOHYD 2118 2118

FT CARBOHYD 2137 2137

FT CARBOHYD 2144 2144

FT CARBOHYD 2155 2155

FT CARBOHYD 2160 2160

FT CARBOHYD 2272 2272

FT CARBOHYD 2430 2430

FT CARBOHYD 2452 2452

FT CARBOHYD 2538 2538

SQ SEQUENCE 3034 AA; 330477 MW; EEF38180AF5ED8A8 CRC64;

Query Match 24.98; Score 59.5; DB 1; Length 3034;

Best Local Similarity 28.64; Pred. No. 16;

Matches 14; Conservative 4; Mismatches 18; Indels 13; Gaps 2;

Qy 4 QCSONEYFDSLHACIPCOL-----RCSNTPPLTCO---RYCN 39

Db 2001 QCKENYKPPAQDACLPDCEPHGSHSRACMDMGQACAPGYIGRCN 2049

RESULT 11
ICEL_ASCSU STANDARD: PRT; 63 AA.
AC P07851;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chymotrypsin/elastase iso1inhibitor 1 (C/E-1 inhibitor).
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OC NCBI_TaxID=6253;
RN 11;
RP MEDLINE=84255715; PubMed=6564898;
RT Babin D.R., Peanasky R.J., Coos S.M.;
RT "The iso1inhibitors of chymotrypsin/elastase from Ascaris
lumbricoides: the primary structure.";
RT Arch. Biochem. Biophys. 232:143-161(1984).
RL 12;
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
RX MEDLINE=95006335; PubMed=7922044;
RA Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
RT "The molecular structure of the complex of Ascaris
chymotrypsin/elastase inhibitor with porcine elastase.";
RT Structure 2:679-689(1994).
CC -1- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.
CC -1- SIMILARITY: BELONGS TO THE ASCARIS TRYPsin INHIBITOR FAMILY.
DR PIR: S07127; S07127.
DR PDB: 1EAI; 05-APR-99.
DR InterPro: IPR002919; T1L_Cys-rich.
DR Pfam: PF01826; T1L: 1.
KM Serine protease inhibitor; 3D-structure.
FT DISULFID 5 38
FT DISULFID 14 33
FT DISULFID 17 29
FT DISULFID 21 60
FT DISULFID 40 54
FT ACT SITE 31 32
SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;
REACTIVE BOND.
Query Match 24.3%; Score 58; DB 1; Length 63;
Best Local Similarity 36.6%; Pred. No. 0.73;
Matches 15; Conservative 5; Mismatches 13; Indels 8; Gaps 4;
QY 5 CSONEYFDSLHACIPQALRC--SSNTP-PLTCOR-YCNAS 41
DB 5 CGPNEVWTE---CTGCEMKCGPDENTPCPLMCRPSCGCS 41
RESULT 12
FUR2_DROME STANDARD: PRT; 1680 AA.
ID FUR2_DROME
AC P30432;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
GN FUR2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=92381036; PubMed=1512259;
RA Redbroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Rantrop M., Garleff E.A.F., Leunissen J.A.M., van de Ven W.J.;
RT "Cloning and functional expression of Drosophila furin-like
proteolytic processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RT J. Biol. Chem. 267:17208-17215(1992).

CC -1- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTIDASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Release of mature proteins from their
CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-1-Zaa bonds, where Xaa
CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
CC complement component C3 and von Willebrand factor from their
CC respective precursors.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: M94375; AAA28551.1; -.
DR PIR: A43434; A43434.
DR HSSP: Q99405; 1MPT.
DR MEROPS: S08.049; -.
DR FLYBase: FBgn0004598; Fur2.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002884; P-domain.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam: PF00082; Peptidase_S8; 1.
DR Pfam: PF01483; P; PARTIAL.
DR PRINTS: PR00723; SUBTILISIN.
DR ProDom: PD000717; P-domain; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00261; FU; 10.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
KM Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane;
KW Multigene family; Zymogen; Repeat.
FT SIGNAL 1 2
FT PROPEP 319
FT CHAIN 320 1680
FT ACT_SITE 418 418
FT ACT_SITE 457 457
FT ACT_SITE 638 638
FT DOMAIN 962 1444
FT REPEAT 962 1007
FT REPEAT 1008 1057
FT REPEAT 1058 1104
FT REPEAT 1105 1153
FT REPEAT 1154 1205
FT REPEAT 1206 1254
FT REPEAT 1255 1299
FT REPEAT 1300 1346
FT REPEAT 1347 1393
FT REPEAT 1394 1444
FT TRANSMEM 1508 1532
FT DOMAIN 1533 1680
FT CARBOHYD 3
FT CARBOHYD 109
FT CARBOHYD 130
FT CARBOHYD 203
FT CARBOHYD 443
FT CARBOHYD 481
FT CARBOHYD 481
FT CARBOHYD 928
FT CARBOHYD 1061
FT CARBOHYD 1182
FT CARBOHYD 1275
FT CARBOHYD 1276
FT CARBOHYD 1440
SQ SEQUENCE 1680 AA; 183599 MW; 0A93CE8770A8E293 CRC64;
Query Match 24.1%; Score 57.5; DB 1; Length 1680;
Best Local Similarity 34.3%; Pred. No. 16;

	Matches	12;	Conservative	5;	Mismatches	17;	Indels	1;	Gaps	16;
OY	5 CSONEYFDSLHLACIPQRCSS-WTPPLTQCORYC	38								
Dt	11:: :::	:								
Dd	1199 CSESEFYSQVEGQCRPCCHASCSCSGCMGPADTSCTSC	1233								
	RESULT_13									
ID	YB40_HUMAN	STANDARD:	PRT:	708 AA.						
Ac	Q9ULTO;									
Dt	16-OCT-2001 (Rel. 40, Created)									
Dt	16-OCT-2001 (Rel. 40, Last sequence update)									
Dt	15-JUN-2002 (Rel. 41, Last annotation update)									
DE	Hypothetical protein KIAA1140 (Fragment).									
GN	KIAA1140.									
OS	Homo sapiens (Human).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.									
OX	NCBI_TaxID=9606;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	TISSUE=Brain;									
RX	MEDLINE=20039618; PubMed=10574461;									
RA	Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,									
RT	"Characterization of cDNA clones selected by the Genemark analysis from size-fractionated cDNA libraries from human brain."									
RL	DNA Res. 6:329-336(1999).									
CC	-1 SIMILARITY: CONTAINS 8 TPR REPEATS.									
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CC	EMBL; AB032966; BAA86454.1; -									
DR	InterPro; IPR001440; TPR.									
DR	Pfam; PF00515; TPR; 7.									
DR	SMART; SMO0028; TPR; 3.									
FK	Hypothetical protein; Repeat; TPR repeat.									
FT	NON_TER REPEAT	1 27								
FT	REPEAT	60								
FT	REPEAT	297								
FT	REPEAT	264								
FT	REPEAT	347								
FT	REPEAT	383								
FT	REPEAT	416								
FT	REPEAT	595								
FT	REPEAT	630								
FT	REPEAT	662								
FT	REPEAT	663								
SQ	SEQUENCE 708 AA; 79140 MM; 8893440BS222CFCLC CRC64; Query Match 23.8%; Score 57; DB 1; Length 708; Best Local Similarity 36.8%; Pred. No. 8.7; Matches 14; Conservative 6; Mismatches 16; Indels 2; Gaps 1.									
OY	5 CSONEYFDSLHLACIPQLRCSNPPTLCGRXCNASV	42								
Dt	1::	: :	:	:	:	:	:	:	:	
Dd	277 CGKSATVAWSLARECV--KLRFSDPVPVLMAAVKVGIGSL	312								
	RESULT_14									
ID	GAS3_ARATH	STANDARD:	PRT:	99 AA.						
Ac	P46877;									
Dt	01-NOV-1995 (Rel. 32, Created)									
Dt	01-NOV-1995 (Rel. 32, Last sequence update)									
Dt	16-OCT-2001 (Rel. 40, Last annotation update)									
DE	Giberellin-regulated protein 3 precursor.									
GN	GASA3 OR ATAG09600 OR T2SP22.40.									

OS Arabidopsis thaliana (Mouse-ear cress).
OC Embryophyta: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
OC eustrods II: Brassicales: Brassicaceae: Arabidopsis.
OX NCBI_TaxId=3702;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueler C., Wambolt R., Murphy G., Volckaert G.,
RA Poll T., Duetschhoef A., Stiekema W., Entlan K.-D., Terryn N.,
RA Harris B., Anstorge W., Brandt P., Glivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chung T.-J., Vandenussche F.,
RA Braeken M., Welfjens I., Voet M., Bastiaens I., Aert R., Defoer E.,
RA Melzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolman S., Klein lankhorst R., Rose M., Hauf J., Koeter P.,
RA Bernelsner S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
RA De Keyser A., Blyssnaert C., Gieten J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., Molay K., Mayes R.,
RA Petteret A., Rajendram M.A., Lyne M., Benes V., Rechmann S.,
RA Borikova D., Blockeier H., Scharfe F., Grimm M., Loehner T.H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Thuer S.,
RA Gabel C., Fuchs W., Fattmann B., Granderath K., Dauner D., Herzi A.,
RA Neumann S., Argirion A., Vitale D., Liqurt R., Piravandi E.,
RA Massenot O., Quigley F., Glabaud C., Muendlein A., Felber R.,
RA Schnabel S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedford F., Cooke R., Berger C., Monfort A., Cascuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez A., Punelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijman D., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,
RA Frijman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedbia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Thneideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Mink P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Krimer J., Fulton L., Mardis E., Darte M., Pepin K., Hillier L.,
RA Nelson J., Spielh J., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidané M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong Y., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granal S., Shohay N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.";
RL Nature 402:769-777(1999).
CC
CC -1- FUNCTION: INVOLVED IN LATE STAGES OF SEED MATURATION, OR IN EARLY
CC STEPS OF GERMINATION.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- TISSUE SPECIFICITY: SLUDGES AND DRY SEEDS.
CC
CC -1- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
CC
CC -1- SIMILARITY: BELONGS TO THE GASTI FAMILY.
CC
CC
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Wed Nov 13 10:41:35 2002

us-09-848-271-2_copy_4_45.rsp

Page 14

```
OY      5 CSQNEYFDLLHACIP-CQ---LRCSNTPLTCORYC 38
       || : : : :||| :| : | ||| :
Db     1851 CSAHSVYTSCVPSCILPSCQPEGGCTGAGAPSPICEGC 1888
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Search completed: November 12, 2002, 16:59:01
Job time : 5.60515 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:16 : Search time 12.7983 Seconds
(without alignments)
676.183 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45
Perfect score: 239
Sequence: 1 MACQSCQNEVFDSLHACIP.....LRCCSNTPPLTCORCNCASV 42

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_21:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mhc:*
8: sp.mammal:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.podent:*
13: sp.virus:*
14: sp.vertibrate:*
15: sp.unclassified:*
16: sp.virus:*
17: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	30.3	499	11	088714
2	69.5	29.1	5374	11	Q99ND0
3	68	28.5	718	5	Q9BI07
4	66	27.6	966	5	Q22378
5	65	27.2	2551	4	Q8WQ08
6	63	26.4	175	11	Q8R4W8
7	63	26.4	341	11	Q9D351
8	61.5	25.7	1299	5	Q26489
9	60.5	25.3	353	5	Q9VW81
10	60.5	25.3	353	5	Q8S258
11	60	25.1	5146	6	Q8SPM4
12	59.5	24.9	548	5	Q9G045
13	59.5	24.9	3034	11	Q35161
14	59	24.7	62	5	Q77419
15	59	24.7	330	5	Q18118
16	59	24.7	937	5	Q9GYS5

17	59	24.7	1717	5	Q26566	Q26566 schistosoma
18	58.5	24.5	798	5	Q9VFR9	Q9VFR9 drosophila
19	58	24.3	532	5	Q17496	Q17496 ascaris suu
20	58	24.3	1513	5	Q17970	Q17970 caenorhabd
21	57.5	24.1	1376	5	Q8S252	Q8S252 drosophila
22	57.5	24.1	1679	5	Q24301	Q24301 drosophila
23	57	23.8	321	10	Q9MAM0	Q9MAM0 arabidopsis
24	57	23.8	387	13	Q9PYD4	Q9PYD4 xenopus lae
25	57	23.8	450	4	Q9BUS3	Q9BUS3 homo sapien
26	57	23.8	502	5	Q17692	Q17692 caenorhabd
27	57	23.8	653	10	Q9S9J8	Q9S9J8 arabidopsis
28	57	23.8	752	4	Q9C091	Q9C091 homo sapien
29	57	23.8	838	5	Q27422	Q27422 caenorhabd
30	57	23.8	838	5	Q18761	Q18761 caenorhabd
31	57	23.8	955	4	Q96DN2	Q96DN2 homo sapien
32	57	23.8	1511	5	Q9VB21	Q9VB21 drosophila
33	56.5	23.6	146	12	Q9EP28	Q9EP28 hepatitis c
34	56.5	23.6	1792	13	Q57484	Q57484 gallus gall
35	56.5	23.6	2820	5	Q9VLR6	Q9VLR6 drosophila
36	56	23.4	260	10	Q8R284	Q8R284 oryza sativ
37	56	23.4	2972	5	P90891	P90891 caenorhabd
38	55.5	23.2	146	12	Q9EP23	Q9EP23 hepatitis c
39	55.5	23.2	225	5	Q9VE40	Q9VE40 drosophila
40	55.5	23.2	675	10	Q94LU3	Q94LU3 oryza sativ
41	55.5	23.2	881	10	Q94LU6	Q94LU6 oryza sativ
42	55.5	23.2	989	10	Q9ZU00	Q9ZU00 arabidopsis
43	55.5	23.2	2843	4	Q9Y6R7	Q9Y6R7 homo sapien
44	55	23.0	160	5	Q9N9Q8	Q9N9Q8 leishmania
45	55	23.0	263	15	Q9WEJ8	Q9WEJ8 human immun

ALIGNMENTS

RESULT 1	ID	AC	Q88714	PRELIMINARY:	PRT:	499 AA.
DT	01-NOV-1998	(TRENBLUREL.08, Created)				
DT	01-NOV-1998	(TRENBLUREL.08, Last sequence update)				
DT	01-JUN-2002	(TRENBLUREL.21, Last annotation update)				
DE	Gastric mucin-like protein (Fragment).					
GN	GASTRIC MUCIN-LIKE.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
FN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=STOMACH;..					
RA	Rio M.C.;					
RA	Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,					
RT	Identification of interactions between trefoil peptides and members					
RT	of the mucin protein family using the yeast two-hybrid system."					
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.					
DR	EMBL	AL010752	CAA09343.1	..		
DR	HSSP	P56682	1CCV			
DR	InterPro	IPR002919	TTL_Cysrich			
DR	InterPro	IPR001846	VWF_D			
DR	Pfam	PF01826	TTL_1			
DR	Pfam	PF00094	WVD_1			
DR	SMART	SM00216	WVD_1			
FT	NON_TER	1				
FT	NON_TER	499				
FT	NON_TER	499				
SO	SEQUENCE	499 AA	54190 MW	04F89EFAF23EE61E CRC64;		
Query Match	30.3%: Score 72.5; DB 11; Length 499;					
Best Local Similarity	48.3%: Pred. No. 0.013; 7; Indels 7; Gaps 1;					
Matches 14: Conservative	1; Mismatches 7; Indels 7; Gaps 1;					
QY	5 CSONEYFDSLHACIPCOLRCCSNTPPLT 33					
DB	430 CSONEYFDSLHACIPCOLRCCSNTPPLT 451					

RESULT 2

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Q99ND0          PRELIMINARY;      PRT: 5374 AA.
ID  Q99ND0
AC  Q99ND0.
DT  01-JUN-2001 (TREMBlrel. 17, Created)
DT  01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT  01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE  ZAN (Conadhesin).
GN  ZAN.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129/SV.
RX  MEDLINE=21138439; PubMed=11239002;
RA  Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA  Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsai L.-C.,
RA  Miller W., Koop B.F.;
RT  "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT  chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL  Nucleic Acids Res. 29:1352-1365(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129/SV.
RA  Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RT  "Genomic Basis of Inter- and Intra-species Variation in Zonadhesin
RT  Domain Structure.";
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
DR  EMBL: AF312033; AAK28824.1; -.
DR  EMBL: AY046056; AAL04416.1; -.
DR  MGD: MG1:106656; ZAN.
DR  InterPro: IPR000561; EGF-like.
DR  InterPro: IPR003645; FOLN.
DR  InterPro: IPR000998; MAM_domain.
DR  InterPro: IPR003328; TILA_Cysrich.
DR  InterPro: IPR002919; TIL_Cysrich.
DR  InterPro: IPR001007; VWF_C.
DR  InterPro: IPR001846; VWF_D.
DR  Pfam: PF00629; MAM; 3.
DR  Pfam: PF01826; TIL; 25.
DR  Pfam: PF02345; TIL; 25.
DR  Pfam: PF00094; wvd; 4.
DR  SMART: SM00001; EGF_Like; 1.
DR  SMART: SM00274; FOLN; 21.
DR  SMART: SM00137; MAM; 3.
DR  SMART: SM00214; VMC; 25.
DR  SMART: SM00216; VMD; 4.
DR  PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR  PROSITE: PS00186; EGF_2; 18.
DR  PROSITE: PS50060; MAM_2; 3.
DR  EGF-like domain; Glycoprotein.
SQ  SEQUENCE 5374 AA; 579536 MW; 90D2D8CFE5DE24EB CRC64;

Query Match          29.1%; Score 69.5; DB 11; Length 5374;
Best Local Similarity 36.8%; Pred. No. 0.37;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;
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RESULT 3

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Q9B107          PRELIMINARY;      PRT: 718 AA.
ID  Q9B107
AC  Q9B107.
DT  01-JUN-2001 (TREMBlrel. 17, Created)
DT  01-JUN-2001 (TREMBlrel. 17, Last sequence update)
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DT  01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE  Putative cysteine surface protein (Fragment).
GN  CSP.
OS  Entamoeba histolytica.
OC  Eukaryota; Entamoebidae; Entamoeba.
CC  NCBI_TaxID=5759;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=HM1:IMSS;
RX  MEDLINE=21428166; PubMed=11545438;
RA  Willhoeft U., Campos-Gongora E., Touznil S., Bruchhaus I., Tannich E.;
RT  "Introns of Entamoeba histolytica and Entamoeba dispar.";
RL  Protist 152:149-156(2001).
DR  EMBL: AJ409106; CAC34072.1; -.
DR  InterPro: IPR002174; Furin-Like.
DR  SMART: SM00261; FU; 7.
FT  NON_TER
SO  SEQUENCE 718 AA; 80231 MW; FFF6362A49F2827A CRC64;
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Query Match          28.5%; Score 68; DB 5; Length 718;
Best Local Similarity 28.6%; Pred. No. 0.09;
Matches 12; Conservative 6; Mismatches 24; Indels 0; Gaps 0;
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RESULT 4

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Q22378          PRELIMINARY;      PRT: 966 AA.
ID  Q22378
AC  Q22378.
DT  01-NOV-1996 (TREMBlrel. 01, Created)
DT  01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT  01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE  Hypothetical 102.5 kDa protein.
GN  t10E10.4.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
CC  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RX  MEDLINE=99069613; PubMed=9851916;
RA  None;
RT  "Genome sequence of the nematode C. elegans: a platform for
RT  investigating biology. The C. elegans Sequencing Consortium.";
RL  Science 282:2012-2018(1998).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RA  Geisler C.;
RT  "The sequence of C. elegans cosmid T10E10.";
RL  Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RA  Waterston R.;
RT  "Direct Submission.";
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL: U39644; AAA80360.2; -.
DR  HSSP: P10969; IMGT.
DR  InterPro: IPR002557; Chitin_bind_Pera.
DR  InterPro: IPR000794; Ketocycl-synt.
DR  InterPro: IPR003571; Snake_toxin.
DR  InterPro: IPR002899; WRI/EB.
DR  Pfam: PF01607; CBM_14; 2.
DR  SMART: SM00289; WRI; 12.
DR  PROSITE: PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR  PROSITE: PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW  Hypothetical protein.
SQ  SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;
```



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026489
ID 026489 PRELIMINARY: PRT: 1299 AA.
AC 026489;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Endoprotease furin.
GN FURIN.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Amphipylinae; Spodoptera.
OX NCBI_TaxId=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SF9;
RA Clepik M., Klek H.;
RT "Cloning and functional characterization of FURIN from Spodoptera
RT frugiperda (SF9) cells."
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z68888; CAA93116.1; -.
DR HSP: Q99405; IMP.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR000209; Peptidase_S8.
DR InterPro: IPR002884; P_domain.
DR Pfam: PF01483; P_1.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR PRODOM: PD000717; P_domain; 1.
DR SMART: SM00261; FU_10.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
DR SMART: SM00494; Chltd2; 3.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 25.7%; Score 61.5; DB 5; Length 1299;
Best Local Similarity 37.5%; Pred. No. 1.5;
Matches 15; Conservative 6; Mismatches 10; Indels 9; Gaps 3;

QY 5 CSQNEFYFDSLHACIPQCLRC-----SNTPLTCORYN 39
DB 1150 CSRPLRLIDLNOCVPC---CSERGVTNSTPPDC-CHCN 1185

RESULT 9
09YW81 PRELIMINARY: PRT: 353 AA.
AC 09YW81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG7348 protein.
GN CG7348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutten G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-T., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dursin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpun G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moberly C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Welschbach J.,
RA Williams S.M., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003514; AAP49068.1; -.
DR Flybase: Fgn0035940; CG7348.
DR InterPro: IPR002557; Chltdn_Bind_Pera.
DR Pfam: PF01607; Chltdn_Bind_Pera.
DR SMART: SM00494; Chltd2; 3.
KW SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;

Query Match 25.3%; Score 60.5; DB 5; Length 353;
Best Local Similarity 31.1%; Pred. No. 0.61;
Matches 14; Conservative 5; Mismatches 15; Indels 11; Gaps 2;

QY 4 QCSQNEFYFDSLHACIPQCL-----RCSNTP-----PLTCORY 37
DB 118 KCSQNVTFDPARRACLPVAISAHGCSCVLPDMATLANPSDCETY 162

RESULT 10
08S258 PRELIMINARY: PRT: 353 AA.
AC 08S258;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RE16222P.
GN CG7348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarini H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclet J., Pargacs V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Cealniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY071103; AAL48725.1; -.
SQ SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;

Query Match 25.3%; Score 60.5; DB 5; Length 353;
Best Local Similarity 31.1%; Pred. No. 0.61;

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DB InterPro: IPR002350: kaza)

DR PROSITE; PS50268; CADHERIN_2; 9

DR PROSITE; PS00022; EGF_1; UNKNOWN_6.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS50227; G-PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G-PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
KW Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein;
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 3034
FT SEQUENCE 3034 AA; 330477 MW; EFP38180AF5ED8A8 CRC64;
SO SEQUENCE 3034 AA; 330477 MW; EFP38180AF5ED8A8 CRC64;
Query Match 24.9%; Score 59.5; DB 11; Length 3034;
Best Local Similarity 28.6%; Pred. No. 6.9;
Matches 14; Conservative 4; Mismatches 18; Indels 13; Gaps 2;
OY 4 QCSONEYFDSLHACIPQL-----RCSSNTPPLTCQ-----RYCN 39
DB 2001 QCKENYKPPADACLPDCDFPHGSHSHACMDTGGCACRFGVIGROCN 2049
RESULT 14
077419
ID 077419 PRELIMINARY; PRT: 62 AA.
AC 077419;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Chymotrypsin/elastase inhibitor-1 (Fragment).
GN ASC/E-1.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
RP Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_Taxid=6253;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98297373; PubMed-9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RT "Anisakis simplex: mutational bursts in the reactive site centers of
RT serine protease inhibitors from an ascarid nematode.";
RL Exp. Parasitol. 89:257-261(1998).
DR EMBL: U94499; AAC61300.1; -.
DR HSP, P07851; IEAI.
DR InterPro: IPR002919; TIL-Cysrich.
DR Pfam: PF01826; TIL; 1.
FT NON_TER 1
FT NON_TER 62
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;
Query Match 24.7%; Score 59; DB 5; Length 62;
Best Local Similarity 35.7%; Pred. No. 0.19;
Matches 15; Conservative 6; Mismatches 13; Indels 8; Gaps 4;
OY 4 QCSONEYFDSLHACIPQLRCS--SNTP-PLTCQR-YCNMS 41
DB 4 RCGPNEVWTE---CTGCEMKCGDPENTPCLMCRPSCCS 41
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ID 018118 PRELIMINARY; PRT: 330 AA.
AC 018118;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE T23F1.6 protein.
GN T23F1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z81129; CAB03405.1; -.
DR InterPro: IPR003341; DUF139.
DR Pfam: PF02363; DUF139; 7.
SQ SEQUENCE 330 AA; 36605 MW; F04381A90D3A8FE9 CRC64;
Query Match 24.7%; Score 59; DB 5; Length 330;
Best Local Similarity 28.9%; Pred. No. 0.96;
Matches 13; Conservative 7; Mismatches 17; Indels 8; Gaps 2;
OY 5 CSONEYFDSLHACIP-----QLRCSNTPPL---TCORYCNMS 41
DB 59 CASSOQYOLQTSQCMFACQSCS00CQSNNTNTQCPFCQSCQTS 103

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Job time : 14.7983 secs